

IDENTIFYING DRUGS FOR AND DIAGNOSIS OF BENIGN PROSTATIC HYPERPLASIA USING GENE EXPRESSION PROFILES

INVENTORS: WILLIAM E. MUNGER, PRAKASH KULKARNI, ROBERT H. GETZENBERG, IWAO WAGA AND JUN YAMAMOTO

RELATED APPLICATIONS

This application claims priority of U.S. Provisional Application No. 60/223,323, filed August 7, 2000, and U.S. Application No. 09/873,319, filed June 5, 2001, which are herein incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

Benign Prostatic Hyperplasia (BPH) is the most common benign tumor in men aged >60 years. It is estimated that one in four men living to the age of 80 will require treatment for this disease. BPH is usually noted clinically after the age of 50, the incidence increasing with age, but as many as two thirds of men between the ages of 40 and 49 demonstrate histological evidence of the disease.

The anatomic location of the prostate at the bladder neck enveloping the urethra plays an important role in the pathology of BPH, including bladder outlet obstruction. Two prostate components are thought to play a role in bladder outlet obstruction. The first is the relative increased prostate tissue mass. The second component is the prostatic smooth muscle tone.

The causative factors of BPH in man have been intensively studied. See Ziada *et al.*, *Urology*, 53: 1-6, 1999. In general, the two most important factors appear to be aging and the presence of functional testes. Although these factors appear to be key to the development of BPH, both appear to be nonspecific.

Little is known about the molecular changes in prostate cells associated with the development and progression of BPH. It has been demonstrated that the expression levels of a number of individual genes are changed compared to normal prostate cells. These changes in gene expression include decreased expression of Wilm's tumor gene (WT-1) and increased expression of insulin growth factor II (IGF-II) (Dong *et al.*, *J. Clin. Endocrin. Metab.*, 82(7): 2198-220).

While the changes in the expression levels of a number of individual genes have been identified, the investigation of the global changes in gene expression has not been reported. Accordingly, there exists a need for the investigation of the changes in global gene expression levels as well as the need for the identification of new molecular markers 5 associated with the development and progression of BPH. Furthermore, if intervention is expected to be successful in halting or slowing down BPH, means of accurately assessing the early manifestations of BPH need to be established. One way to accurately assess the early manifestations of BPH is to identify markers which are uniquely associated with disease 10 progression. Likewise, the development of therapeutics to prevent or stop the progression of BPH relies on the identification of genes responsible for BPH growth and function.

SUMMARY OF THE INVENTION

The present invention is based on the elucidation of the global changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate 15 hyperplasia as compared to normal prostate tissue as well as the identification of individual genes that are differentially expressed in BPH tissue.

The invention is also based on the discovery of a means of effectively selecting disease-linked drug targets from gene expression results. The invention includes methods of classifying genes whose expression levels are changed in diseased tissues, during disease 20 induction or during disease progression into specific groups. By using this method it is possible to classify genes whose expression are regulated by the same mechanism into the same group, and it is possible to identify representative marker genes by selecting typical genes from each cluster.

The invention includes methods of screening for or identifying an agent that modulates the onset or progression of BPH, comprising: preparing a first gene expression 25 profile of BPH cells; exposing the cells to the agent; preparing a second gene expression profile of the agent exposed cells; and comparing the first and second gene expression profiles. In a preferred embodiment of these methods, the gene expression profile comprises the expression levels of one or more or preferably two or more genes in Tables 1-6. In another preferred embodiment of these methods, the cell is a prostate cell from a BPH 30 patient, a cell line in Table 7, or a derivative thereof.

The invention also includes methods of monitoring a treatment of a patient with BPH, comprising administering a pharmaceutical composition to the patient; preparing a gene expression profile from a prostate cell or tissue sample from the patient; and comparing the patient gene expression profile to a gene expression profile from a normal prostate cell population, a BPH tissue or BPH cells without treatment with the pharmaceutical composition. In preferred embodiments of these methods, the gene expression profile comprises the expression levels of one or more or, preferably two or more genes in Tables 1-6.

The invention also includes methods of diagnosing benign prostatic hyperplasia (BPH) in a subject comprising the step of detecting the level of expression in a tissue or cell sample from the subject of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH progression.

The invention further includes methods of detecting the onset or progression of benign prostatic hyperplasia (BPH) in a patient comprising the step of detecting the level of expression in a tissue or cell sample of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH progression.

The invention also includes methods of differentiating benign prostatic hyperplasia (BPH) from prostate cancer in a patient comprising the step of detecting the level of expression in a tissue or cell sample of two or more genes from Tables 1-6 (preferably Tables 3-5, and more preferably Table 5); wherein differential expression of the genes is indicative of BPH rather than prostate cancer.

The invention also includes methods of selecting or identifying cells that can be used for drug screening.

All of these methods may include the step of detecting the expression levels of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10 or more genes in any of Tables 1-6, or preferably Table 5. In a preferred embodiment, expression of all of the genes or nearly all of the genes in Tables 1-6, or preferably Table 5, may be detected.

The invention further includes sets of at least two or more probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-6 as well as solid supports comprising at least two or more of the probes.

The invention also includes computer systems comprising or linked to a database containing information identifying the expression level in BPH tissue or cells of a set of genes comprising at least two genes in Tables 1-6, preferably from Table 5; and a user interface to view the information. The database may further comprise sequence information for the genes as well as information identifying the expression level for the set of genes in normal prostate tissue or cells, and prostate cancer tissue. The database may further contain or be linked to descriptive information from an external database, which information correlates said genes to records in the external database.

The invention further includes methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one of the genes in Tables 1-6, preferably Table 5, comprising comparing the expression level of at least one gene in Tables 1-6, preferably Table 5, in the tissue or cell to the level of expression of the gene in the database.

Lastly, the invention includes kits comprising probes or solid supports of the invention. In some embodiments, the kits also contain written materials or software concerning gene expression information for the genes of the invention, preferably in electronic format.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Figure 1 shows the expression of cellular retinol binding protein RNA in various tissues.

Figure 2. Figure 2 shows the expression of cellular retinol binding protein RNA in various prostate tissues samples. In all of the figures, "Normal", "-Sym", "Cancer" and "+Sym" refer to normal prostate, BPH without symptoms, prostate cancer, and BPH with symptoms, respectively.

Figure 3. Figure 3 shows the expression of S100 calcium binding protein RNA in various tissues.

Figure 4. Figure 4 shows the expression of S100 calcium binding protein RNA in various prostate tissue samples.

Figure 5. Figure 5 shows the expression of human prostate-specific membrane antigen (PSMA) RNA in various tissues.

5 Figure 6. Figure 6 shows the expression of PSMA RNA in various prostate tissue samples.

Figure 7A-7C. Figure 7A shows a 3-dimensional view of the results of a Preferred Component Analysis (PCA) comparing BPH patients with symptoms (S), asymptomatic BPH patients (O), asymptomatic BPH patients with prostate cancer (C) and normal control subjects (N). Figure 7B shows the same PCA in a 2-dimensional format plotting component 10 1 versus components 2+3. The patients are depicted here as: BPH patients with symptoms (BPHWS), asymptomatic BPH patients (BPHNoS), asymptomatic BPH patients with prostate cancer (Cancer) and normal control subjects (Normal). Figure 7C depicts the same data as 15 Figure 7B, with the addition of two additional normal (Norm) and three additional BPH patients with symptoms (BPH).

DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (e.g. through control of initiation, provision of RNA precursors, 20 RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression 25 of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, Cell, 64: 313-326 (1991); Weinberg, Science, 254:1138-1146 (1991)). Thus, changes in the expression levels of particular genes (e.g. oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during 30 drug screening development. Often drugs are screened for the ability to interact with a major

target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue from normal prostate, BPH and BPH prostate tissue immediately adjacent to malignant prostate tissue to identify the global changes in gene expression in BPH. These changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, toxicity, drug efficacy and drug metabolism.

10 **Assay Formats**

The genes identified as being differentially expressed in BPH tissue or BPH cells (Tables 1-6) may be used in a variety of nucleic acid detection assays to detect or quantitatively the expression level of a gene or multiple genes in a given sample. For example, traditional Northern blotting, nuclease protection, RT- PCR and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention, particularly when smaller numbers of genes are assayed. For instance, when fewer than 50 genes are assayed, RT-PCR techniques can be used to prepare high-throughput assays. However, methods and assays of the invention are most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

20 Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based beads or chips, etc. Such supports and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used.

30 A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or

400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any technique known in the art (see for example, Lockhart *et al.*, *Nat. Biotechnol.* (1996) 14, 1675-1680; McGall *et al.*, *Proc. Nat. Acad. Sci. USA* (1996) 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-6. For instance, such arrays may contain oligonucleotides that are complementary or hybridize to at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70 or more of the genes described herein.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not. The genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with less processing steps.

The sequences and related information of the genes described herein are available in the public databases. Tables 1-6 provide the Accession numbers and name for each of the sequences. Each Accession Number corresponds to a sequence in the attached sequence listing. The sequences and related information of the genes listed in the Tables according to their GenBank identifiers are expressly incorporated herein as of the filing date of this application, as are sequences in the databases related to those herein described, such as fragments, variant sequences, etc. (see: www.ncbi.nlm.gov).

Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for interrogating the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-6 refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at

the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

“Bind(s) substantially” refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms “background” or “background signal intensity” refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, *etc.*). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.* probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack probes.

The phrase “hybridizing specifically to” refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular DNA or RNA).

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 different nucleic acid hybridizations.

As used herein a “probe” is defined as a nucleic acid molecule, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical

bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization.

5 Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent

10 conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least

15 about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or

20 span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.* nucleic acid base or amino acid residue) occurs in both sequences to yield the

25 number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

30 *Probe design*

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes could be oligonucleotides that range from about 5 to about 500 or 5 to about 45 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect (the genes of Tables 1-6).

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence

intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to an actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls or mismatch probes may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For

example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

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Nucleic Acid Samples

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process.

Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes*, Part I Theory and Nucleic Acid Preparation, P. Tijssen, Ed., Elsevier, N.Y. (1993). Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised in vitro, such as cell lines and tissue culture cells. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes. Frequently, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to prostate tissue, urine, sputum, blood, blood-cells (e.g., white cells or peripheral blood leukocytes (PBL), tissue or fine needle biopsy samples, peritoneal fluid, and pleural fluid, or cells therefrom.

Forming High Density Arrays.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling. See Pirrung *et al.*, U.S. Patent No. 5,143, 854.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary.

Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is 5 performed at low stringency in this case in 6X SSPE-T at 37°C (0.005% Triton X-100) to ensure hybridization and then subsequent washes are performed at higher stringency (e.g., 1 X SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25 X SSPET at 37°C to 10 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e.g., expression level control, normalization control, mismatch controls, *etc.*).

In general, there is a tradeoff between hybridization specificity (stringency) and signal 15 intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between 20 each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels 25 attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

Databases

The present invention includes relational databases containing sequence information, 30 for instance for the genes of Tables 1-6, as well as gene expression information in various prostate tissue samples. Databases may also contain information associated with a given

sequence or tissue sample such as descriptive information about the gene associated with the sequence information, metabolic pathway information for the gene or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. Such information for the patient may include, but is not limited to sex, age, disease 5 status, general health information, surgical or treatment status, PSA levels, as well as information concerning the patient's clinical symptoms. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for instance, see U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

10 The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 1-6, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

15 Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available 20 from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

25 The databases of the invention may be used to produce, among other things, electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

20 The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least two of the genes in Tables 1-6, comprising the step of comparing the expression level of at least one gene in Tables 1-6 found or detected in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the hyperplastic state of a given tissue by comparing the level of expression of a gene or genes in Tables 1-6 from a sample to the expression levels found in normal prostate cells, BPH cells or tissue and/or malignant or 30 cancerous prostate tissue. Such methods may also be used in the drug or agent screening assays as described below.

Selection of BPH-Associated Genes

BPH associated genes may be identified or selected by any available method, including subtractive hybridization protocols, differential display protocols and high-throughput hybridization formats, including oligonucleotide and cDNA microarray technologies.

Unprocessed or raw expression levels may be normalized, standardized and/or analyzed by any available computational method, including the expression level normalization, analysis and clustering methods herein described. The normalization method as described in Example 4 may be combined with any further analysis method, including any clustering methods available in the art.

Diagnostic Uses for the BPH Markers

As described above, the genes and gene expression information provided in Tables 1-6 may be used as diagnostic markers for the prediction or identification of the hyperplastic state of a prostate or other tissue. For instance, a prostate tissue or other patient sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-6 may be compared to the expression levels found in normal prostate tissue, BPH tissue or BPH tissue from a patient with metastatic or nonmetastatic prostate cancer. In some instances, patient PBLs may be used as the patient sample. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the BPH Markers for Monitoring Disease Progression

As described above, the genes and gene expression information provided in Tables 1-6 may also be used as markers for the monitoring of disease progression, such as the development of BPH. For instance, a prostate tissue or other patient sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-6 may be compared to the expression levels found in normal prostate tissue, BPH tissue or BPH tissue from a patient with metastatic or nonmetastatic prostate cancer. The

comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

The BPH markers of the invention may also be used to track or predict the progress or 5 efficacy of a treatment regime in a patient. For instance, a patient's progress or response to a given drug may be monitored by creating a gene expression profile from a tissue or cell sample after treatment or administration of the drug. The gene expression profile may then be compared to a gene expression profile prepared from normal cells or tissue, for instance, 10 normal prostate tissue. The gene expression profile may also be compared to a gene expression profile prepared from BPH or malignant prostate cells, or from tissue or cells from the same patient before treatment. The gene expression profile may be made from at least 15 one gene, preferably more than one gene, and most preferably all or nearly all of the genes in Tables 1-6.

15 *Use of the BPH Markers for Drug Screening*

According to the present invention, the genes identified in Tables 1-6 can be used as 20 markers to screen for potential therapeutic agents or compounds to treat BPH or prostate cancer. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or to down-regulate or counteract the transcription or expression of a marker or markers. Compounds that modulate the expression 25 level of single gene and also compounds that modulate the expression level of multiple genes from levels associated with a specific disease state to a normal state can be screened by using the markers and profiles identified herein.

According to the present invention, one can also compare the specificity of drug's 25 effects by looking at the number of markers which are differentially expressed after drug exposure and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 1-6 may 30 utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a

nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least 2 genes from Tables 1-6 may be used to directly monitor or detect changes in gene expression in the treated or 5 exposed cell as described in more detail above. In another format, the changes of mRNA expression level can be detected using QuantiGene technology (Warrior *et. al.* (2000) *J. Biomolecular Screening*, 5, 343-351). Specific probes used for QuantiGene can be designed and synthesized to one or more genes from Tables 1-6. Cells treated with compounds are lysed by lysis buffer. The amount of target mRNA can be detected as a luminescence 10 intensity using target specific probes.

In another format, cell lines that contain reporter gene fusions between the open reading frame and/or 5'/3' regulatory regions of a gene in Tables 1-6 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol 15 acetyltransferase (Alam *et al.* (1990) *Anal. Biochem.* 188:245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent 20 and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate 25 the expression of a gene identified in Tables 1-6. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Laboratory Press, 1989).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically (see below). Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of 30 modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, prostate derived. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector)

construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag or some other detectable marker or tag. Such a process is well known in the art (see Maniatis).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e.g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample is then compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-6. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, *etc.* An 5 example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or 10 rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, 15 vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure 20 chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant GA. in: Meyers (ed.) Molecular Biology and Biotechnology (New York, VCH Publishers, 1995), pp. 659-664). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Cells used for Multi Gene Screening

Many kinds of cells such as primary cells and cell lines can be used for the drug 25 screening methods of the invention. Cells or cell lines derived from prostatic tissues are preferred because the innate gene expression mechanisms of these cells often resemble those of prostatic tissues. Cells used for drug screening can be selected by assaying for the expression of one or more of the marker genes listed in Tables 1-6. The cells which differentially express one or more, or preferably nearly all of the marker genes listed in 30 Tables 1-6 are preferred cells or cell lines for the methods of the invention (see Table 7).

Kits

The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to diagnose the disease state of a tissue or cell sample, to monitor the progression of prostate disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

The databases packaged with the kits are a compilation of expression patterns from human and laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-6). In particular, the database software and packaged information include the expression results of Tables 1-6 that can be used in the assays and methods as herein described. In another format, database access is provided to the purchaser or user through an electronic means, *e.g.*, via the Internet or by direct dial-in access.

The kits may be used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

Databases and software designed for use with microarrays is discussed in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables, collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the genes, chips, *etc.* of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

5

EXAMPLES

Example 1: Gene chip expression analysis

Human tissue was obtained from the transitional zone of the prostate (the junction 10 between the ejaculatory duct and the prostatic urethra) in biopsy samples from normal individuals and from patients with BPH or prostate cancer. BPH was defined histologically 15 in all samples. Normal tissue and asymptomatic BPH samples came from individuals who died of trauma and did not report symptoms. Because BPH is a disease associated with aging, two groups of normal individuals were identified, group 1, ages 20 or under, and group 20 2, ages 30-50. Patients having BPH with symptoms were defined as those with a need for frequent urination. In these patients, a radical prostatectomy had been performed. Prostate 25 cancer patients provided age-matched tissue samples for symptomatic BPH patients, but were without symptoms and without cancer in the transitional zone under histological examination.

Microarray sample preparation was conducted with minor modifications, following 20 the protocols set forth in the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 µg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded 25 cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 µg/ml. From 2 µg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript *in vitro* 30 Transcription Kit.

To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol

(Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix Human 42K array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were 5 washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard 10 Gene Array Scanner). Data was analyzed using Affymetrix GeneChip version 3.0 and Expression Data Mining Tool (EDMT) software (version 1.0).

Differential expression of genes between the BPH and normal prostate samples were determined using the Affymetrix GeneChip human gene chip set by the following criteria: 1) For each gene, Affymetrix GeneChip average difference values were determined by standard Affymetrix EDMT software algorithms, which also made "Absent" (=not specifically detected as gene expression), "Present" (=detected) or "Marginal" (=not clearly Absent or Present) calls for each GeneChip element; 2) all AveDiff values which were less than +20 (positive 20) were raised to a floor of +20 so that fold change calculations could be made where values were not already greater than or equal to +20; 3) median levels of expression were compared between the normal control group and the BPH with symptoms disease group 20 to obtain greater than or equal 2-fold up/down values; 4) The median value for the higher expressing group needed to be greater or equal to 200 average difference units in order to be considered for statistical significance; 5) Genes passing the criteria of #1-4 were analyzed for statistical significance using a two-tailed T test and deemed statistically significant if $p < 0.05$. Tables 1 and 2 list the genes and their levels of differential expression (compared to 25 normal samples) in BPH tissue from patients with symptoms of BPH and in BPH tissue immediately adjacent to malignant prostate tissue isolated from male patients.

Example 2 : Expression profile analysis

Gene expression profiles between normal sample and BPH patient samples were 30 determined by using the following samples: 10 normal; 7 BPH without symptoms; 8 BPH with cancer; and 8 BPH with symptoms. Gene expression profiles were prepared using the

42K Affymetrix Gene Chip set. The methods used were the same as described in Example 1 with the exception of the criteria to select the marker genes.

The criteria used in this study were as follows; 1) For each gene, Affymetrix GeneChip average difference values were determined by standard Affymetrix EDMT software algorithms, which also made "Absent" (=not specifically detected as gene expression), "Present" (=detected) or "Marginal" (=not clearly Absent or Present) calls for each GeneChip element; 2) all AveDiff values which were less than +20 (positive 20) were raised to a floor of +20 so that fold change calculations could be made where values were not already greater than or equal to +20; 3) mean levels of expression were compared between the normal control group and the BPH with symptoms disease group; 4) genes were arranged by the fold change starting with the largest one (Fold change calculation was determined by using logarithmic values in Example 2); and 5) the top 200 up-regulated genes and bottom 200 down-regulated genes were selected. The genes identified in this study are listed in Tables 3 (normal vs. BPH with symptoms, up regulated) and 4 (normal vs. BPH with symptoms, down regulated, values are negative fold-change from normal).

Example 3 : Selection of Cell lines used for Multi Gene Screening

A number of cultured cell lines were tested to determine the similarity in gene expression profiles to BPH tissue. Cells were cultured in 6-well plates using the appropriate medium for each cell line. After reaching 90% confluence, cells were lysed with Trizol (GiboBRL) and total RNA was extracted. mRNA was then isolated, cDNA and cRNA was synthesized, and gene expression levels were determined by the Affymetrix Human 42K Gene Chip set as described in more detail above.

The gene expression profiles were compared with those of prostatic tissue samples. A panel of 61 genes whose expression levels were up-regulated in BPH with symptoms compared with normal samples and with small variation among samples (within BPH samples and within normal samples) were assayed. The group of genes whose signal intensity was more than 100 in each cell line is summarized in Table 1. A panel of 43 genes whose expression levels were down-regulated in BPH patient with small variation among samples was also assayed. The group of genes whose signal intensity in Affymetrix Gene Chip was "Present call" is also included in Table 1. Similarly, genes whose expression level

is up- or down-regulated in patients with BPH and cancer, compared to normal controls, are listed in Table 2.

Forty-eight to 58% of genes applied for this analysis were expressed in the cell lines of Table 7. These results indicate that cell lines, BRF-55T (Biological Research Faculty & Facility Inc.), PZ-HPV7 (ATCC; CRL-2221), BPH-1 (S.W. Hayward *et al.*, *In Vitro Cell Dev. Biol.* 31A, 14-24, 1995) and LNCaP (ATCC; CRL-1740) can be used as a BPH – like cell population to screen for compounds which are capable of modulating gene expression profiles from the disease state to a normal state using the genes of Tables 1-6. In particular, BRF-55T is a useful cell line for screening in the assays of the invention, because 58% genes of the assayed genes were differentially expressed in BRF-55T as compared to BPH with symptoms tissue.

Example 4 : Cluster analysis of up- or down-regulated genes in BPH

Cluster analysis of the expression results from a large number of genes is often problematic due to variations in the standardization of the gene expression data. To compensate for these variations, a subset of differentially expressed genes was selected by a modified analysis procedure.

In a first step, a gene list comparing normal vs. disease samples was generated by two kinds of comparisons. First, genes were selected that displayed a greater than or equal to mean 2-fold up or down regulation using average difference expression values and with $p < 0.05$. Second, genes were selected by ANOVA comparing the normal group of samples with the disease group and with a *t* value of > 3 in the up or down direction. These lists were then combined to create an expression profile characteristic of normal controls and one characteristic of disease in which specific genes are found to be up or down regulated in disease when compared with normal controls.

In preparation for clustering analysis to identify subgroups of genes that show statistically similar expression patterns, average difference values for the selected genes were normalized across all samples (normal and disease combined) using the following formula:

$$\text{Normalization data} = (X - X_{\text{mean}})/S_x$$

Where S_x is variance ($:STD$)

This converts the mean expression value for each gene to 0 and the high and low values to 1 and -1, respectively. Thus, genes with high absolute expression values when compared with genes with low absolute expression values would not skew the comparisons when clustering algorithms are applied.

5 The measurement of the cluster space distance was determined by using the correlation coefficient (1-r) method and clustering was performed using Ward's method (Ward,J.H. (1963) *Journal of American Statistical Association*, 58. 236.)

The clustering was validated by observing whether multiple elements representing the same genes showing the same direction of expression change (*i.e.*, either up or down) tend to cluster together. To test this standardization and clustering protocol, the expression levels for genes that are represented by more than one element on the 42K gene chip set were analyzed to determine whether the multiple elements for a single gene could be clustered together. For example, tryptase, also known as alpha tryptase or beta (tryptase II) is represented by two separate elements on the 42K human gene chip. This gene is registered with 2 different element names 41268 (5), M33493_s_at (code name, Up-170) and 26389 (3), rc_AA131322_s_at (code name, Up-010).

It was found that the best analysis means for decreasing measurement errors between these two elements is by the Ward method as it gave the most consistent results when compared to other clustering methods. These analysis methods may be incorporated into 20 software or computer readable storage media for storing a computer programmer software.

Example 5 : Selection of 60 Marker Genes

A panel of 60 representative marker genes (listed in Table 5) out of 400 marker genes listed in Tables 3 and 4 can be used in the assays and methods of the invention. The 60 marker genes were selected based on following criteria: (1) expression level is changed greatly in BPH patient samples compared with normal samples; (2) variation of expression levels within BPH samples and within normal samples is small; and (3) expression levels resembling BPH with symptoms are detected in cell line BRF-55T.

Example 6: Gene Expression Analysis of Select Genes

The expression levels of three genes from Tables 1-5 (the genes encoding cellular retinol binding protein, S100 calcium binding protein and PSMA) were assayed in various tissues and prostate samples by PCR as described in Example 7 (see Figures 1-6). Each sample was assayed for the level of GAPDH and mRNA corresponding to cellular retinol binding protein, S100 calcium binding protein or PSMA. As seen in Figures 1-6, these three genes are differentially regulated or expressed in BPH tissue from patients with or without symptoms and from BPH tissue from patients with prostate cancer (compared to normal prostate tissue). All three genes are therefore useful markers in the assays of the invention, such as the assays to measure the effect of an agent on BPH or the assays to detect or 10 diagnose the occurrence or progression of BPH.

Example 7: Drug Screening Assays

The expression profiles for normal controls and disease samples described above can be used to identify compound hits from a compound library. A hit may be, but is not 15 necessarily, defined as one of three kinds of results:

- 1) The expression of an individual gene is changed in the direction of normal (*i.e.*, if up in disease, then down=hit, if down in disease, then up=hit). The stronger the modulation of an individual gene to a normal phenotype, the stronger the hit status for the compound against that gene.
- 20 2) The expression of genes that subcluster together is evaluated for an overall pattern of modulation to a normal expression profile. The more genes in a subcluster that are modulated to a normal phenotype, the stronger the hit status for the compound against that subcluster. A subcluster may represent common or interacting cellular pathways.
- 25 3) The overall expression profile of all of the genes being screened is evaluated for modulation to normal. The more genes that are modulated to a normal phenotype, the stronger the hit status for the compound against the entire gene set.

As described above, if a compound modulates the gene expression pattern of the screening system cells more towards any disease phenotype, then it can be used as a molecular probe to find binding proteins and/or define disease-associated cellular pathways.

30 As an example, candidate agents and compounds are screened for their ability to modulate the expression levels of cellular retinol binding protein, S100 calcium binding

protein and PSMA by exposing a prostate cell line or cell line from BPH tissue to the agent and assaying the expression levels of these genes by real time PCR. Real time PCR detection is accomplished by the use of the ABI PRISM 7700 Sequence Detection System. The 7700 measures the fluorescence intensity of the sample each cycle and is able to detect the 5 presence of specific amplicons within the PCR reaction. Each sample is assayed for the level of GAPDH and mRNA corresponding to cellular retinol binding protein, S100 calcium binding protein and PSMA. GAPDH detection is performed using Perkin Elmer part#402869 according to the manufacturer's directions. Primers were designed for the three genes by 10 using Primer Express, a program developed by PE to efficiently find primers and probes for specific sequences ((1) N91971 - FAM PROBE Forward: 5'- CAT ggC TTT gTT TTA AgA AAA ggA A -3'; Reverse: 5'- AgC CAC CCC CAg gCA T -3'; Probe: 5'-FAM - AgT gAC AAA gCC AAg AgA CAg ACT CTg CTA ACA - TAMRA-3'; (2) X65614 – SYBR; Forward: 5'- AAA gAC AAg gAT gCC gTg gAT -3'; Reverse 5'-AgC CAC gAA CAC gAT gAA CTC-3'; (3) M99487-SYB; Forward 5'-Tgg CTC AgC ACC ACC Aga T-3'; Reverse: 15 5'-TTC Cag TAA AgC Cag gTC CAA-3')

These primers are used in conjunction with SYBR green (Molecular Probes), a nonspecific double stranded DNA dye, to measure the expression level mRNA corresponding to the genes, which is normalized to the GAPDH level in each sample.

Normalized expression levels from cells exposed to the agent are then compared to 20 the normalized expression levels in control cells. Agents that modulate the expression of one or more the genes may be further tested as drug candidates in appropriate BPH *in vitro* or *in vivo* models.

Example 8: Comparative assays

25 The expression of a panel of marker genes was compared, in the same subjects as disclosed in Example 2, in a pairwise fashion between the BPH patients with (BPHWS) or without (BPHNoS) symptoms versus normal (Normal) controls and asymptomatic BPH patients with cancer (Cancer). In every case, the tissue was excised from the junction between the ejaculatory duct and the prostatic urethra in the transition zone of the prostate. In 30 particular, BPH tissue from patients with early stage prostate cancer was carefully excised away from the cancer lesion macroscopically, and their histological diagnosis was confirmed microscopically.

Pairwise comparisons between the subject groups were subjected to an Analysis of Variance (ANOVA) model. P-values corresponding to each of six possible pairwise comparisons among the four sample groups were then determined for each gene. Table 6 depicts Affymetrix fragments, along with their GenBank accession number, which have p<0.001 for two or more of the pairwise comparisons.

A Principal Component Analysis (PCA) was performed to show that this gene set serves as a basis to discriminate among the various groups of samples. The samples are plotted using the scores for the first three principal components. Each of the four sample groups can be clearly distinguished from one another in this analysis (Figure 7A).

Component 1 (36% of the variability) discriminates between Normal and asymptomatic BPH versus BPH cancer and symptomatic BPH. Component 2 (10% of the variability) distinguishes Normal from asymptomatic BPH, and Component 3 (8% of the variability) distinguishes BPH cancer from symptomatic BPH.

Figure 7B shows a two-dimensional representation of the PCA, with Component 1 plotted against Components 2 + 3. Each of the four sample groups is clustered in a different quadrant of this figure. Within each sample group, there does not appear to be any age-related clustering of samples. Further, since there is an overlap of ages between the samples groups, it does not appear that age was a confounding factor for the analysis based on this gene set. Because BPH is perceived as a natural consequence of aging, two subgroups of normal individuals were initially identified. A 'younger' set included individuals ranging in age from 13-20 years while the 'older' set ranged from 31-51 years. However, because the two subsets appeared to be indistinguishable at the molecular level, they were grouped together and in all subsequent analysis referred to as 'Normal' group.

Another finding was that the intra-group variability (*i.e.*, the tightness of clustering) differed between the four groups (Figure 7A). Normal patients exhibited the least intra-group variability, followed by asymptomatic BPH and symptomatic BPH with BPH cancer patients exhibiting the most patient-to-patient variability. On the other hand, with regard to the inter-group variation, the asymptomatic BPH group appeared to be more similar to the normal group than to symptomatic BPH (Figure 7B).

Asymptomatic BPH samples were obtained from individuals that died from other causes and had no records of being treated for BPH but had histological evidence for BPH when examined retrospectively. Since asymptomatic samples clearly exhibit the BPH phenotype at the microscopic level, one would expect the two BPH groups to exhibit more

similarity than disparity. Similarly, that the BPH cancer group is distinct from asymptomatic BPH but is more similar to the symptomatic BPH group (Figure 7B). Since transition zone tissue from patients with prostate cancer with no clinical symptoms of BPH was analyzed from these patients, this group of patients would be expected to appear similar to normal or 5 asymptomatic BPH. The fact that the BPH cancer group can be distinguished from every other group is also an unexpected finding. Subsequent to this PCA, additional samples were studied to extend these findings. These included two normals and three symptomatic BPH patients. Using the same set of genes, a PCA was performed with these additional samples. In Figure 7C, the two new normal (Norm) samples group with the previous normal samples 10 and the three new symptomatic BPH (BPH) samples group with the other symptomatic BPH samples.

Example 9: Diagnostic assays

The expression profiles or one or more of the individual genes of Tables 1-6 are used 15 as molecular or diagnostic markers to evaluate the disease status of a patient sample. In one embodiment, a patient prostate tissue sample is processed as described herein to produce total cellular or mRNA. The RNA is hybridized to a chip containing probes that specifically hybridize to one or more, or two or more of the genes in Tables 1-6. The overall expression profile generated, or the expression levels of individual genes are then compared to the 20 profiles as described in Tables 1-6 to determine the disease or hyperplastic state of the patient sample.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing 25 from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, applications, GenBank Accession numbers and publications referred to in this application are herein incorporated by reference in their entirety.

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_AA463726_s_at | 386 | AA463726 | JM27 proteinXp11.23 | 14.9 | 0.018598344 |
| RC_AA057195_at | 47 | AA057195 | Homo sapiens mRNA; cDNA DKFZp586M121 (from clone DKFZp586M121) | 14.0 | 0.029325045 |
| V01512_rna1_at | 993 | V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 13.1 | 0.001027561 |
| RC_AA427622_s_at | 311 | AA427622 | collagen, type XIII, alpha 110q22 | 11.6 | 0.00074954 |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 11.4 | 0.000631487 |
| RC_AA465491_at | 391 | AA465491 | Mad4 homolog4p16.3 | 11.4 | 0.031024189 |
| RC_AA620825_at | 454 | AA620825 | ESTs | 11.3 | 0.010915901 |
| RC_R93908_at | 865 | R93908 | ESTs | 11.3 | 0.019994337 |
| RC_AA461300_at | 381 | AA461300 | ESTs | 11.0 | 0.007061759 |
| N40141_at | 743 | N40141 | JM27 proteinXp11.23 | 10.9 | 0.013756347 |
| RC_R25410_at | 814 | R25410 | ESTs | 7.7 | 0.01851753 |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 7.4 | 0.041523744 |
| RC_AA279760_at | 193 | AA279760 | ESTs | 7.0 | 0.024411468 |
| RC_T90889_at | 927 | T90889 | ESTs | 6.5 | 0.015666863 |
| U62015_at | 978 | U62015 | insulin-like growth factor binding protein 101p22-p31 | 6.0 | 0.002843661 |
| RC_AA188981_at | 112 | AA188981 | highly expressed in cancer, rich in leucine heptad repeats | 5.9 | 0.002280479 |
| D83018_at | 513 | D83018 | nel (chicken)-like 212q13.11-q13.12 | 5.6 | 0.000570952 |
| RC_H64493_f_at | 590 | H64493 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 5.6 | 0.01109802 |
| X52541_at | 1064 | X52541 | early growth response 15q31.1 | 5.2 | 0.002428259 |
| M57466_s_at | 690 | M57466 | major histocompatibility complex, class II, DP beta 16p21.3 | 5.1 | 0.002137399 |
| J03507_at | 621 | J03507 | complement component 75p13 | 4.9 | 1.36616E-05 |
| RC_N30198_at | 733 | N30198 | ESTs | 4.8 | 0.003366461 |
| RC_T78398_at | 913 | T78398 | EST | 4.8 | 0.033293747 |
| RC_H17550_at | 559 | H17550 | ESTs | 4.7 | 0.047828622 |
| RC_T67053_f_at | 909 | T67053 | immumoglobulin lambda gene cluster22q11.1-q11.2 | 4.5 | 0.045107075 |
| RC_AA598982_s_at | 429 | AA598982 | trophininXp11.22-p11.21 | 4.3 | 0.000902336 |
| RC_AA256268_at | 175 | AA256268 | ESTs | 4.2 | 0.001506239 |
| HG3543-HT3739_at | 675 | M29645 | insulin-like growth factor 2 (somatomedin A)11p15.5 | 4.1 | 0.017253126 |
| RC_N91971_f_at | 791 | N91971 | retinol-binding protein 1, cellular3q23 | 4.1 | 0.02528773 |
| RC_AA479286_at | 403 | AA479286 | ESTs | 4.0 | 0.028009544 |
| M62831_at | 695 | M62831 | immediate early protein19 | 4.0 | 0.000484086 |
| RC_F02992_at | 526 | F02992 | ESTs, Weakly similar to unknown [M.musculus] | 3.9 | 0.031845412 |
| RC_H86112_f_at | 600 | H86112 | KIAA0471 gene product1q24-q25 | 3.8 | 0.004155259 |
| RC_AA436616_at | 335 | AA436616 | ESTs | 3.8 | 0.017156387 |
| RC_T62857_at | 903 | T62857 | ESTs | 3.7 | 0.000301735 |
| RC_AA281345_f_at | 201 | AA281345 | immediate early protein19 | 3.6 | 0.001679723 |
| U21128_at | 953 | U21128 | lumican12q21.3-q22 | 3.6 | 2.19529E-05 |
| U30521_at | 960 | U30521 | P311 protein | 3.6 | 0.001150397 |
| RC_N58172_at | 757 | N58172 | ESTs | 3.5 | 0.043092144 |
| RC_T03229_f_at | 874 | T03229 | EST | 3.5 | 0.031101935 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| X06700_s_at | 1049 | X06700 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)2q31 | 3.5 | 0.008472599 |
| RC_Z39904_at | 1111 | Z39904 | Homo sapiens clone 23555 mRNA sequence | 3.4 | 0.002949046 |
| RC_T23622_at | 886 | T23622 | ESTs | 3.4 | 0.002174281 |
| J00231_f_at | 617 | J00231 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 3.4 | 0.009322568 |
| RC_AA028092_s_at | 17 | AA028092 | transcription factor 216pter-qter | 3.4 | 3.13963E-06 |
| RC_AA252528_at | 170 | AA252528 | ESTs | 3.4 | 0.000225707 |
| L33799_at | 645 | L33799 | procollagen C-endopeptidase enhancer7q22 | 3.3 | 0.018469201 |
| RC_F09748_s_at | 537 | F09748 | Homo sapiens mRNA; cDNA DKFZp586K1220 (from clone DKFZp586K1220) | 3.2 | 0.02728166 |
| RC_T64223_s_at | 907 | T64223 | carboxypeptidase A3 (mast cell)3q21 q25 | 3.2 | 0.027915742 |
| RC_AA402903_f_at | 263 | AA402903 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 3.2 | 0.044721116 |
| RC_F13763_at | 542 | F13763 | ESTs | 3.1 | 0.000503701 |
| RC_AA488432_at | 412 | AA488432 | phosphoserine phosphatase7p21-p15 | 3.1 | 0.020997503 |
| RC_AA486072_i_at | 410 | AA486072 | small inducible cytokine A5 (RANTES)17q11.2-q12 | 3.1 | 0.025877597 |
| RC_N22006_s_at | 719 | N22006 | EST | 3.1 | 0.00148561 |
| RC_AA257093_r_at | 178 | AA257093 | T-cell receptor, beta cluster7q35 | 3.1 | 1.71945E-07 |
| RC_AA609943_at* | 449 | AA609943 | ESTs | 3.0 | 0.029360518 |
| RC_T23490_s_at | 885 | T23490 | ESTs | 3.0 | 0.008741411 |
| D13628_at | 476 | D13628 | angiopoietin 18q22.3-q23 | 2.9 | 0.006228419 |
| M73720_at | 702 | M73720 | carboxypeptidase A3 (mast cell)3q21 q25 | 2.9 | 0.006585391 |
| Z74616_s_at | 1123 | Z74616 | collagen, type I, alpha 27q22.1 | 2.8 | 0.008750622 |
| AA082546_at | 54 | AA082546 | ESTs | 2.8 | 0.019771126 |
| RC_AA284920_at | 213 | AA284920 | ESTs | 2.7 | 0.019738239 |
| RC_AA599365_at | 434 | AA599365 | decorin12q23 | 2.7 | 0.001295936 |
| X57025_at | 1066 | X57025 | insulin-like growth factor 1 (somatomedin C)12q22-q23 | 2.7 | 0.022341194 |
| X51345_at | 1062 | X51345 | jun B proto-oncogene19p13.2 | 2.7 | 0.036487159 |
| RC_N67876_s_at | 773 | N67876 | insulin-like growth factor 1 (somatomedin C)12q22-q23 | 2.7 | 0.035216134 |
| RC_AA609504_at | 444 | AA609504 | KIAA0405 gene product | 2.7 | 0.020881055 |
| RC_N69207_at | 776 | N69207 | ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens] | 2.6 | 0.041315387 |
| M87789_s_at | 704 | M87789 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 2.6 | 0.038916248 |
| HG3510-HT3704_at | 1055 | X12795 | nuclear receptor subfamily 2, group F, member 15q14 | 2.6 | 0.016151338 |
| RC_T64211_at | 906 | T64211 | ESTs, Weakly similar to pancortin-1 [M.musculus] | 2.6 | 0.006233291 |
| U90552_s_at | 988 | U90552 | butyrophilin, subfamily 3, member A16p23 | 2.6 | 0.004564282 |
| M34516_r_at | 684 | M34516 | immunoglobulin lambda-like polypeptide 322q11.2 | 2.6 | 0.049767038 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|---|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_T23468_at | 884 | T23468 | ESTs | 2.5 | 0.00250737 |
| RC_AA173223_at | 108 | AA173223 | ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | 2.5 | 0.007080285 |
| RC_T49061_at | 894 | T49061 | ESTs | 2.5 | 0.039642391 |
| RC_AA234095_at | 144 | AA234095 | ESTs | 2.5 | 0.003152859 |
| RC_F01920_s_at | 520 | F01920 | pre-B-cell leukemia transcription factor 39q33-q34 | 2.5 | 0.002088945 |
| RC_N91461_at | 789 | N91461 | ESTs | 2.4 | 0.01015467 |
| RC_N67575_s_at | 771 | N67575 | osteoglycin (osteoinductive factor) | 2.4 | 0.004044061 |
| RC_AA151210_at | 89 | AA151210 | ESTs | 2.4 | 0.011476541 |
| AA156897_s_at | 97 | AA156897 | Homo sapiens mRNA; cDNA DKFZp564I1922 (from clone DKFZp564I1922) | 2.4 | 0.033974981 |
| W73859_at | 1028 | W73859 | transcription factor 216pter-qter | 2.4 | 0.024640626 |
| RC_H68097_at | 592 | H68097 | EST | 2.4 | 0.04870874 |
| RC_AA436618_at | 336 | AA436618 | ESTs | 2.4 | 0.02483165 |
| M33493_s_at | 680 | M33493 | tryptase, beta (tryptase II)16p13.3 | 2.4 | 0.02689938 |
| AB002340_at | 461 | AB002340 | KIAA0342 gene product | 2.3 | 0.000748796 |
| RC_AA446661_at | 347 | AA446661 | ESTs | 2.3 | 0.011980248 |
| RC_AA084138_at | 55 | AA084138 | ESTs | 2.3 | 1.16025E-05 |
| RC_N59866_at | 761 | N59866 | ESTs, Weakly similar to putative p150 [H.sapiens] | 2.3 | 0.002042263 |
| RC_R42424_at | 832 | R42424 | ESTs | 2.3 | 0.003173074 |
| RC_N39415_at | 742 | N39415 | osteoglycin (osteoinductive factor) | 2.3 | 0.001310764 |
| J03464_s_at | 620 | J03464 | collagen, type I, alpha 27q22.1 | 2.3 | 0.006791534 |
| RC_AA205376_at | 121 | AA205376 | KIAA0471 gene product1q24-q25 | 2.3 | 0.023123837 |
| RC_H95960_at | 606 | H95960 | secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32 | 2.3 | 0.008509182 |
| D28137_at | 484 | D28137 | bone marrow stromal cell antigen 219p13.2 | 2.3 | 0.031127266 |
| RC_N79778_at | 784 | N79778 | extracellular matrix protein 2, female organ and adipocyte specific9q22.3 | 2.3 | 0.045073744 |
| RC_N98485_s_at | 800 | N98485 | forkhead (Drosophila)-like 66p25.3 | 2.3 | 0.033372862 |
| M98539_at | 715 | M98539 | prostaglandin D2 synthase (21kD, brain)9q34.2-q34.3 | 2.2 | 0.005442674 |
| RC_AA205724_at | 123 | AA205724 | ESTs | 2.2 | 0.006183612 |
| U85625_at | 986 | U85625 | Homo sapiens ribonuclease 6 precursor, mRNA, complete cds. | 2.2 | 0.001245066 |
| RC_R37588_s_at | 821 | R37588 | RAB2, member RAS oncogene family-like6p21.3 | 2.2 | 0.00219386 |
| RC_AA046426_at | 35 | AA046426 | Cdc42 effector protein 3 | 2.2 | 0.005788723 |
| RC_AA256294_at | 176 | AA256294 | ESTs | 2.2 | 0.002425605 |
| RC_AA599120_at | 431 | AA599120 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 | 2.2 | 0.042979241 |
| RC_W60186_at | 1018 | W60186 | ESTs | 2.2 | 0.028494835 |
| RC_AA599216_at | 432 | AA599216 | collapsin response mediator protein 14p16.1-p15 | 2.2 | 0.040523744 |
| RC_AA450324_at | 360 | AA450324 | ESTs | 2.1 | 0.009094567 |
| M31994_at | 678 | M31994 | Homo sapiens aldehyde dehydrogenase (ALDH1) gene | 2.1 | 0.001561218 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_AA402930_at | 264 | AA402930 | ESTs | 2.1 | 0.000114627 |
| M91029_cds2_at | 706 | M91029 | Human AMP deaminase isoform L (AMPD2) mRNA, exons 6-18, partial cds | 2.1 | 0.02494373 |
| RC_AA450114_at | 358 | AA450114 | ESTs, Weakly similar to 17beta-hydroxysteroid dehydrogenase [H.sapiens] | 2.1 | 4.87556E-06 |
| D62584_at | 501 | D62584 | osteoglycin (osteoinductive factor) | 2.1 | 0.000157116 |
| RC_AA621634_at | 457 | AA621634 | ESTs | 2.1 | 0.02297009 |
| RC_AA312946_s_at | 228 | AA312946 | ESTs | 2.1 | 3.51075E-05 |
| X07438_s_at | 1054 | X07438 | Human DNA for cellular retinol binding protein (CRBP) | 2.1 | 0.039015947 |
| RC_N53447_at | 751 | N53447 | integral membrane protein 2CXq21.1-21.2 | 2.1 | 0.009032297 |
| RC_AA281591_at | 202 | AA281591 | Homo sapiens mRNA; cDNA DKFZp586B211 (from clone DKFZp586B211) | 2.0 | 0.016660714 |
| RC_R71395_at | 854 | R71395 | ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens] | 2.0 | 0.046231847 |
| RC_T53590_s_at | 899 | T53590 | cytochrome P450, subfamily XIA (cholesterol side chain cleavage)15q23-q24 | 2.0 | 0.00282074 |
| RC_AA293489_at | 224 | AA293489 | KIAA0638 protein | 2.0 | 0.006966532 |
| RC_AA447707_s_at | 351 | AA447707 | KIAA1055 protein | 2.0 | 0.001248537 |
| RC_AA235618_f_at | 149 | AA235618 | ESTs | 2.0 | 0.012481746 |
| RC_N68350_at | 775 | N68350 | ESTs | 2.0 | 0.035156598 |
| RC_H81379_s_at | 596 | H81379 | ESTs, Moderately similar to KIAA0438 [H.sapiens] | 2.0 | 0.01148429 |
| RC_D51060_s_at | 495 | D51060 | Jun activation domain binding protein1p32-p31 | 2.0 | 0.016668951 |
| U72649_at | 983 | U72649 | B-cell translocation gene 2 (pheochromacytoma cell-3)1q32 | 2.0 | 0.020660388 |
| RC_AA287389_at | 216 | AA287389 | ESTs | 2.0 | 0.002741873 |
| RC_AA621367_at | 456 | AA621367 | ESTs | 2.0 | 0.004871903 |
| J03040_at | 619 | J03040 | secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32 | 2.0 | 0.006303994 |
| RC_AA291676_s_at | 219 | AA291676 | non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)5q23-q31 | 2.0 | 0.027480479 |
| RC_N63536_at | 763 | N63536 | ESTs | 2.0 | 0.000634305 |
| RC_AA411952_at | 282 | AA411952 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 33q25 | 2.0 | 0.011858934 |
| RC_AA252802_s_at | 171 | AA252802 | Human mRNA for TI-227H | 2.0 | 0.041027635 |
| RC_AA382275_at | 244 | AA382275 | ESTs | 2.0 | 0.00087437 |
| AA093923_at | 63 | AA093923 | tissue inhibitor of metalloproteinase 217q25 | 2.0 | 0.046200886 |
| M11313_s_at | 654 | M11313 | alpha-2-macroglobulin12p13.3-p12.3 | 2.0 | 0.013660595 |
| RC_AA398280_at | 248 | AA398280 | ESTs | 2.0 | 0.044320644 |
| RC_N51529_at | 747 | N51529 | ESTs | 2.0 | 0.006276979 |
| H49440_at | 578 | H49440 | nudix (nucleoside diphosphate linked moiety X)-type motif 36p21.2 | 2.0 | 0.013879331 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_T33263_s_at | 890 | T33263 | KIAA0320 protein | 2.0 | 0.009994615 |
| RC_T89160_r_at | 921 | T89160 | ESTs | 2.0 | 0.005289266 |
| RC_W56792_at | 1016 | W56792 | ESTs, Weakly similar to serine/threonine protein kinase TAO1 [R.norvegicus] | 2.0 | 0.026130523 |
| RC_R60056_at | 849 | R60056 | ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens] | 2.0 | 0.001585076 |
| Down-regulated | | | | | |
| RC_AA398908_at | 251 | AA398908 | Human Chromosome 16 BAC clone CIT987SK-A-61E3 | -21.7 | 0.007918174 |
| RC_AA460914_at | 380 | AA460914 | ESTs | -15.8 | 0.013659536 |
| RC_T40895_at | 892 | T40895 | ESTs | -12.6 | 0.002430219 |
| RC_R71792_s_at | 855 | R71792 | ESTs, Moderately similar to FAT-SPECIFIC PROTEIN FSP27 [M.musculus] | -9.8 | 0.01438632 |
| RC_N80129_i_at | 785 | N80129 | metallothionein 1L16q13 | -8.7 | 0.002816872 |
| X66141_at | 1078 | X66141 | myosin, light polypeptide 2, regulatory, cardiac, slow12q23-q24.3 | -8.0 | 0.03928942 |
| AA234634_f_at | 145 | AA234634 | CCAAT/enhancer binding protein (C/EBP), delta8p11.2-p11.1 | -7.4 | 0.000589696 |
| U78294_at | 985 | U78294 | arachidonate 15-lipoxygenase, second type | -6.8 | 0.017271608 |
| RC_AA457566_at | 375 | AA457566 | ESTs | -6.6 | 0.029644622 |
| X93036_at | 1093 | X93036 | phospholemann-like, expressed in breast tumors, 8kD | -6.2 | 0.011323909 |
| X57129_at | 1067 | X57129 | H1 histone family, member 26p21.3 | -6.1 | 0.004161922 |
| HG1067-HT1067_r_at | 671 | M22406 | Human intestinal mucin mRNA, partial cds, clone SMUC 42 | -5.8 | 0.007202185 |
| X65614_at | 1076 | X65614 | S100 calcium-binding protein P4p16 | -5.8 | 0.006892572 |
| RC_AA609006_at | 440 | AA609006 | ESTs | -5.7 | 0.015701354 |
| J03910_rna1_at | 622 | J03910 | metallothionein 1G16q13 | -5.7 | 0.003506953 |
| RC_H94471_at | 604 | H94471 | occludin5q13.1 | -5.6 | 0.025014274 |
| AB000584_at | 459 | AB000584 | prostate differentiation factor | -5.4 | 0.003235425 |
| RC_W88568_at | 1035 | W88568 | glycogenin 2Xp22.3 | -5.1 | 0.048573115 |
| V00594_at | 992 | V00594 | metallothionein 2A16q13 | -5.0 | 0.000721258 |
| RC_T73433_s_at | 912 | T73433 | angiotensinogen1q41-qter | -4.9 | 0.012700144 |
| RC_N94303_at | 797 | N94303 | ESTs | -4.5 | 4.88059E-05 |
| RC_AA419011_at | 296 | AA419011 | Homo sapiens mRNA; cDNA DKFZp586D0823 (from clone DKFZp586D0823) | -4.1 | 0.013801595 |
| RC_N32748_at | 736 | N32748 | ESTs | -4.1 | 0.018749207 |
| RC_AA053424_at | 40 | AA053424 | ESTs, Weakly similar to mucin Muc3 [R.norvegicus] | -4.0 | 0.001235197 |
| RC_AA599331_at | 433 | AA599331 | ESTs | -4.0 | 0.005480655 |
| M99487_at | 716 | M99487 | folate hydrolase (prostate-specific membrane antigen) 111p11.2 | -3.9 | 0.013268152 |
| RC_F02245_at | 522 | F02245 | monoamine oxidase AXp11.4-p11.3 | -3.8 | 0.002950391 |
| X76717_at | 1087 | X76717 | metallothionein 1L16q13 | -3.7 | 0.000868707 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|---|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| X64177_f_at | 1075 | X64177 | metallothionein 1H16q13 | -3.7 | 0.002089771 |
| RC_AA599522_r_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | -3.6 | 0.012643918 |
| L77701_at | 651 | L77701 | human homolog of yeast mitochondrial copper recruitment gene | -3.6 | 0.003341007 |
| RC_D11824_at | 474 | D11824 | ESTs, Moderately similar to weak similarity to <i>Arabidopsis thaliana</i> ubiquitin-like protein 8 [C.elegans] | -3.6 | 0.000803294 |
| RC_AA410311_at | 275 | AA410311 | ESTs | -3.5 | 0.001234064 |
| RC_AA457235_at | 373 | AA457235 | ESTs | -3.5 | 0.012177965 |
| RC_N93798_at | 796 | N93798 | protein tyrosine phosphatase type IVA, member 3 | -3.5 | 0.007340453 |
| RC_AA416762_s_at | 291 | AA416762 | nuclear receptor subfamily 1, group H, member 219q13.3-19q13.3 | -3.5 | 0.010404304 |
| RC_F03969_at | 528 | F03969 | ESTs, Weakly similar to tumorous imaginal discs protein Tid56 homolog [H.sapiens] | -3.5 | 0.011826812 |
| RC_AA045487_at | 31 | AA045487 | ESTs | -3.4 | 0.025187615 |
| RC_Z38744_at | 1108 | Z38744 | putative gene product13 | -3.4 | 2.30674E-05 |
| RC_N92502_s_at | 794 | N92502 | ESTs, Moderately similar to HERV-E integrase [H.sapiens] | -3.4 | 0.02301359 |
| RC_R91484_at | 863 | R91484 | ESTs | -3.4 | 8.2306E-05 |
| RC_AA165313_at | 104 | AA165313 | ESTs | -3.3 | 0.028364404 |
| RC_AA182030_at | 110 | AA182030 | ESTs | -3.3 | 0.019770486 |
| RC_T94447_s_at | 928 | T94447 | ESTs, Moderately similar to (define not available 4335935) [M.musculus] | -3.3 | 0.001427294 |
| RC_W20486_f_at | 995 | W20486 | ESTs | -3.3 | 0.002892697 |
| RC_R16983_at | 811 | R16983 | ESTs | -3.2 | 0.000912559 |
| RC_AA504805_s_at | 424 | AA504805 | interferon stimulated gene (20kD)15q26 | -3.2 | 0.003905701 |
| RC_T90190_s_at | 925 | T90190 | H1 histone family, member 26p21.3 | -3.2 | 0.020618793 |
| RC_AA135870_at | 79 | AA135870 | ESTs | -3.1 | 0.04609197 |
| RC_H99035_at | 612 | H99035 | ESTs | -3.1 | 0.000191451 |
| RC_R28370_at | 815 | R28370 | ESTs | -3.1 | 0.024606319 |
| RC_T40995_f_at | 893 | T40995 | alcohol dehydrogenase 3 (class I), gamma polypeptide4q21-q23 | -3.1 | 0.024064044 |
| MIP1-B_at | 1124 | M35590 | karyopherin (importin) beta 2 | -3.1 | 0.005882353 |
| RC_AA447522_at | 349 | AA447522 | ESTs, Highly similar to differentially expressed in Fanconi anemia [H.sapiens] | -3.1 | 0.003518059 |
| RC_AA461453_at | 382 | AA461453 | ESTs, Moderately similar to Cab45a [M.musculus] | -3.0 | 0.021949087 |
| AA429539_f_at | 318 | AA429539 | ESTs | -3.0 | 0.017623102 |
| RC_AA476944_at | 394 | AA476944 | ESTs | -3.0 | 0.019974254 |
| RC_N80129_f_at | 785 | N80129 | metallothionein 1L16q13 | -3.0 | 0.000219038 |
| RC_N26904_at | 731 | N26904 | ESTs, Weakly similar to FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens] | -2.9 | 0.006305062 |
| RC_AA505136_at | 426 | AA505136 | ESTs | -2.9 | 0.005400284 |
| AA455001_s_at | 368 | AA455001 | ESTs | -2.9 | 2.1534E-05 |
| RC_W70131_at | 1024 | W70131 | ESTs | -2.9 | 0.005764635 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|---|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_AA043349_at | 27 | AA043349 | ESTs | -2.9 | 0.016983419 |
| U02020_at | 936 | U02020 | pre-B-cell colony-enhancing factor | -2.9 | 0.003324497 |
| U52969_at | 970 | U52969 | Purkinje cell protein 421q22.2-q22.3 | -2.8 | 0.00078638 |
| RC_H22453_at | 564 | H22453 | ESTs | -2.8 | 0.000410695 |
| RC_N22620_at | 722 | N22620 | ESTs | -2.8 | 0.005507089 |
| RC_N64683_at | 764 | N64683 | ESTs | -2.8 | 0.00378977 |
| RC_N24761_at | 725 | N24761 | ESTs | -2.8 | 0.004837185 |
| RC_AA464728_s_at | 388 | AA464728 | ESTs | -2.8 | 0.004669897 |
| RC_H83380_at | 598 | H83380 | ESTs | -2.7 | 0.016543793 |
| M30894_at | 676 | M30894 | T-cell receptor, gamma cluster7p15-p14 | -2.7 | 0.034153167 |
| RC_H81070_f_at | 595 | H81070 | Human metallothionein (MT)I-F gene | -2.7 | 0.022654931 |
| J00073_at | 615 | J00073 | actin, alpha, cardiac muscle15q11-qter | -2.7 | 0.029724167 |
| RC_H05084_at | 547 | H05084 | ESTs, Weakly similar to ORF YDL055c [S.cerevisiae] | -2.7 | 0.016965435 |
| AA045870_at | 34 | AA045870 | Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072) | -2.7 | 0.005480167 |
| RC_T68873_f_at | 911 | T68873 | metallothionein 1L16q13 | -2.7 | 0.001140431 |
| RC_N72253_at | 778 | N72253 | ESTs | -2.7 | 0.001832591 |
| RC_AA447977_s_at | 352 | AA447977 | Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072) | -2.7 | 0.001255304 |
| RC_H18947_at | 561 | H18947 | ESTs | -2.7 | 0.00193501 |
| RC_H77597_f_at | 594 | H77597 | metallothionein 1H16q13 | -2.7 | 0.001560766 |
| RC_H94475_s_at | 605 | H94475 | alpha-2-plasmin inhibitor17pter-p12 | -2.6 | 0.01435663 |
| RC_AA025370_at | 15 | AA025370 | KIAA0872 protein | -2.6 | 0.013924142 |
| RC_AA443114_at | 343 | AA443114 | ESTs, Moderately similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [M.musculus] | -2.6 | 0.000703574 |
| RC_F09684_at | 535 | F09684 | ESTs | -2.6 | 0.000107291 |
| RC_AA031360_s_at | 20 | AA031360 | ESTs | -2.6 | 0.047293081 |
| RC_AA416685_at | 290 | AA416685 | UNC13 (C. elegans)-like9p11-p12 | -2.6 | 0.023296279 |
| D29805_at | 487 | D29805 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 19p13 | -2.6 | 2.3562E-05 |
| RC_H58873_s_at | 583 | H58873 | solute carrier family 2 (facilitated glucose transporter), member 11p35-p31.3 | -2.5 | 0.000710917 |
| M10942_at | 652 | M10942 | metallothionein 1E (functional)16q13 | -2.5 | 0.017370635 |
| RC_T03593_at | 875 | T03593 | ESTs | -2.5 | 0.006239127 |
| RC_N95495_at | 799 | N95495 | small inducible cytokine A5 (RANTES)17q11.2-q12 | -2.5 | 0.002392984 |
| RC_AA017063_r_at | 8 | AA017063 | ESTs, Highly similar to Miz-1 protein [H.sapiens] | -2.5 | 0.048093776 |
| RC_R00144_at | 801 | R00144 | ESTs | -2.5 | 0.018222161 |
| RC_AA599522_f_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | -2.5 | 0.03100833 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_AA219552_s_at | 134 | AA219552 | ESTs | -2.5 | 0.043156485 |
| RC_AA447537_at | 350 | AA447537 | ESTs, Moderately similar to (defline not available 5360237) [M.musculus] | -2.5 | 0.031129269 |
| RC_AA070752_s_at | 51 | AA070752 | insulin receptor substrate 12q36 | -2.5 | 0.002895462 |
| RC_R02003_r_at | 804 | R02003 | ESTs, Weakly similar to cappuccino [D.melanogaster] | -2.4 | 0.002315115 |
| L13698_at | 638 | L13698 | growth arrest-specific 19q21.3-q22.1 | -2.4 | 0.013393145 |
| RC_AA432292_at | 325 | AA432292 | ESTs, Moderately similar to B cell growth factor [H.sapiens] | -2.4 | 0.000956642 |
| RC_H99648_s_at | 613 | H99648 | DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis5q22-q23) | -2.4 | 0.009066307 |
| RC_AA131919_at | 75 | AA131919 | putative type II membrane protein | -2.4 | 0.000187872 |
| RC_AA621695_at | 458 | AA621695 | ESTs | -2.4 | 0.008761556 |
| RC_AA598695_at | 427 | AA598695 | ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] | -2.4 | 0.000549977 |
| RC_AA430388_at | 321 | AA430388 | ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | -2.4 | 0.000135176 |
| M24069_at | 672 | M24069 | cold shock domain protein A12p13.1 | -2.4 | 0.015890231 |
| RC_AA434108_at | 327 | AA434108 | Homo sapiens heat shock protein hsp40-3 mRNA, complete cds | -2.4 | 0.013182623 |
| RC_AA405488_at | 268 | AA405488 | ESTs | -2.3 | 0.015044159 |
| RC_AA419546_at | 297 | AA419546 | ESTs | -2.3 | 0.030432017 |
| RC_W38197_at | | W38197 | EST | -2.3 | 0.013006462 |
| RC_R38709_s_at | 824 | R38709 | superoxide dismutase 2, mitochondrial6q25.3 | -2.3 | 0.03567491 |
| RC_AA121142_at | 69 | AA121142 | ESTs, Moderately similar to copper transport protein HAH1 [H.sapiens] | -2.3 | 0.043639016 |
| RC_N26801_at | 730 | N26801 | ESTs | -2.3 | 0.000580867 |
| RC_N75960_at | 781 | N75960 | ESTs | -2.3 | 0.01244791 |
| RC_R36969_at | 820 | R36969 | ESTs | -2.3 | 0.019129486 |
| AA046840_at | 36 | AA046840 | CCAAT/enhancer binding protein (C/EBP), delta8p11.2-p11.1 | -2.3 | 0.002504544 |
| RC_R46074_at | 840 | R46074 | transforming, acidic coiled-coil containing protein 210q26 | -2.3 | 0.003462273 |
| X06956_at | 1051 | X06956 | tubulin, alpha 1 (testis specific)2q | -2.3 | 0.015437809 |
| RC_H84761_s_at | 599 | H84761 | glutathione peroxidase 13p21.3 | -2.2 | 0.000365528 |
| RC_W52065_f_at | 1012 | W52065 | KIAA0539 gene product | -2.2 | 0.016497348 |
| RC_AA279757_at | 192 | AA279757 | ESTs, Weakly similar to (defline not available 4481810) [D.melanogaster] | -2.2 | 0.003272622 |
| RC_H16676_s_at | 556 | H16676 | ESTs, Weakly similar to (defline not available 5107634) [R.norvegicus] | -2.2 | 8.86866E-05 |
| RC_AA255480_at | 173 | AA255480 | ESTs | -2.2 | 0.009359024 |
| RC_R96924_s_at | 866 | R96924 | ESTs | -2.2 | 0.000201685 |
| RC_AA342337_at | 231 | AA342337 | ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | -2.2 | 0.024999347 |
| RC_AA004699_at | 1 | AA004699 | putative translation initiation factor | -2.2 | 0.022298405 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_AA401965_at | 258 | AA401965 | tumor suppressor deleted in oral cancer-related 111q13 | -2.2 | 0.006294885 |
| RC_F02470_at | 524 | F02470 | Homo sapiens clone 24796 mRNA sequence | -2.2 | 0.022313149 |
| X76180_at | 1086 | X76180 | sodium channel, nonvoltage-gated 1 alpha12p13 | -2.2 | 0.023078001 |
| RC_R49138_s_at | 841 | R49138 | coatomer protein complex, subunit epsilon | -2.2 | 0.020401578 |
| RC_D80237_s_at | 506 | D80237 | actin related protein 2/3 complex, subunit 4 (20 kD) | -2.2 | 0.022022634 |
| RC_AA402224_at | 260 | AA402224 | growth arrest and DNA-damage-inducible, gamma9q22.1-q22.2 | -2.2 | 0.014983528 |
| RC_AA281599_at | 203 | AA281599 | Homo sapiens mRNA for for histone H2B, clone pjG4-5-14 | -2.2 | 0.029567009 |
| RC_N78630_at | 782 | N78630 | KIAA0870 protein | -2.2 | 0.006668895 |
| X85785_rna1_at | 1091 | X85785 | Duffy blood group1q21-q22 | -2.2 | 0.018706507 |
| RC_AA412063_at | 285 | AA412063 | ESTs | -2.2 | 0.000686563 |
| RC_AA022886_at | 14 | AA022886 | ESTs, Weakly similar to phosphatidylinositol transfer protein [H.sapiens] | -2.2 | 0.000777067 |
| RC_N24899_at | 726 | N24899 | ESTs | -2.2 | 0.030610964 |
| RC_AA101767_at | 66 | AA101767 | ESTs | -2.2 | 0.009040467 |
| RC_AA045503_at | 32 | AA045503 | ESTs, Weakly similar to Homo sapiens p20 protein [H.sapiens] | -2.2 | 0.021950966 |
| RC_F10078_at | 538 | F10078 | ESTs | -2.1 | 0.040699115 |
| RC_H02308_at | 545 | H02308 | ESTs | -2.1 | 0.036730715 |
| RC_AA284153_at | 210 | AA284153 | ESTs | -2.1 | 0.021270233 |
| RC_AA453433_at | 363 | AA453433 | HLA-B associated transcript-16p21.3 | -2.1 | 0.013366375 |
| RC_AA403159_at | 265 | AA403159 | Homo sapiens Ste-20 related kinase SPAK mRNA, complete cds | -2.1 | 0.025212073 |
| RC_T17428_s_at | 883 | T17428 | Homo sapiens clone 23836 mRNA sequence | -2.1 | 0.044754602 |
| RC_W92449_at | 1037 | W92449 | ESTs, Highly similar to (defline not available 4587714) [H.sapiens] | -2.1 | 0.019386585 |
| RC_AA609312_at | 443 | AA609312 | ESTs | -2.1 | 0.003204911 |
| D28589_at | 486 | D28589 | Human mRNA (KIAA00167), partial sequence | -2.1 | 0.000408478 |
| RC_AA232508_at | 139 | AA232508 | ESTs, Highly similar to (defline not available 4929647) [H.sapiens] | -2.1 | 0.004626663 |
| RC_AA280929_s_at | 199 | AA280929 | ESTs | -2.1 | 0.028189798 |
| W63793_at | 1020 | W63793 | S-adenosylmethionine decarboxylase 16q21-q22 | -2.1 | 0.032076011 |
| RC_R36881_s_at | 819 | R36881 | Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence | -2.1 | 0.007343473 |
| RC_AA278767_s_at | 188 | AA278767 | ESTs | -2.1 | 0.001983494 |
| RC_R98442_at | 867 | R98442 | ESTs | -2.1 | 0.007227226 |
| X99728_at | 1098 | X99728 | H.sapiens NDUFV3 gene, exon 3. | -2.1 | 0.001404191 |
| RC_R09379_at | 807 | R09379 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13 | -2.1 | 0.006004344 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|---|---------------------------|-----------------------|
| Up-regulated | | | | | 1669617.1 |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_R99092_at | 868 | R99092 | EST, Moderately similar to (defline not available 5052951) [H.sapiens] | -2.1 | 0.016256526 |
| X95325_s_at | 1095 | X95325 | cold shock domain protein A12p13.1 | -2.1 | 0.025953179 |
| RC_T56281_f_at | 902 | T56281 | Human metallothionein (MT)I-F gene | -2.1 | 0.032089569 |
| RC_R44397_at | 835 | R44397 | ESTs | -2.1 | 0.000265391 |
| RC_H27180_f_at | 568 | H27180 | ESTs | -2.1 | 0.004317675 |
| AA165312_at | 103 | AA165312 | ESTs | -2.1 | 0.025559572 |
| RC_AA279313_s_at | 191 | AA279313 | methyl CpG binding protein 2Xq28 | -2.1 | 0.030594523 |
| HG4322-HT4592_at | 465 | AF141349 | Homo sapiens beta-tubulin mRNA, complete cds. | -2.1 | 0.017120749 |
| RC_H81413_f_at | 597 | H81413 | high-mobility group (nonhistone chromosomal) protein isoforms I and Y6p21 | -2.1 | 0.009976588 |
| RC_W94333_at | 1039 | W94333 | ESTs, Highly similar to (defline not available 5107163) [H.sapiens] | -2.1 | 0.000435688 |
| RC_AA455070_at | 369 | AA455070 | eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) | -2.1 | 0.025226928 |
| RC_R11526_f_at | 809 | R11526 | parathyrosin17q12-q22 | -2.1 | 0.027182202 |
| RC_T15409_f_at | 877 | T15409 | EST | -2.1 | 0.001478856 |
| RC_H05625_f_at | 548 | H05625 | ESTs | -2.1 | 0.024564209 |
| RC_AA620461_at | 452 | AA620461 | ESTs | -2.0 | 0.022844667 |
| RC_AA449791_f_at | 356 | AA449791 | EST | -2.0 | 0.025394324 |
| RC_AA435769_s_at | 330 | AA435769 | ESTs | -2.0 | 0.008375153 |
| RC_N55502_at | 755 | N55502 | ESTs | -2.0 | 0.021894439 |
| AF001294_at | 463 | AF001294 | tumor suppressing subtransferable candidate 311p15.5 | -2.0 | 0.03566128 |
| RC_Z40898_at | 1118 | Z40898 | ESTs, Highly similar to (defline not available 4929639) [H.sapiens] | -2.0 | 0.002289892 |
| RC_AA436861_at | 340 | AA436861 | ESTs | -2.0 | 0.00187676 |
| M63573_at | 697 | M63573 | peptidylprolyl isomerase B (cyclophilin B)15 | -2.0 | 0.044239663 |
| RC_T25732_f_at | 888 | T25732 | KIAA0252 protein | -2.0 | 0.041237995 |
| RC_R01257_at | 803 | R01257 | ESTs, Weakly similar to (defline not available 4456991) [H.sapiens] | -2.0 | 0.005735841 |
| RC_H91703_i_at | 603 | H91703 | cell division cycle 2717q12-17q23.2 | -2.0 | 0.001412925 |
| RC_N34817_at | 739 | N34817 | ESTs | -2.0 | 0.040996591 |
| RC_R60777_at | 850 | R60777 | ESTs, Weakly similar to KIAA0374 [H.sapiens] | -2.0 | 0.000245565 |
| RC_AA386264_at | 245 | AA386264 | ESTs, Weakly similar to MICROTUBULE-ASSOCIATED PROTEIN 1B [M.musculus] | -2.0 | 0.000541139 |
| RC_AA251769_at | 168 | AA251769 | ESTs, Weakly similar to Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [H.sapiens] | -2.0 | 0.008985897 |
| RC_R56602_at | 846 | R56602 | Ig superfamily proteinXq12-q13.3 | -2.0 | 0.024051216 |
| RC_AA397919_at | 247 | AA397919 | ESTs | -2.0 | 0.029784087 |

TABLE 1 Normal1-Normal2 vs BPH-With Symptoms

1669617.1

| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-change N1-N2 vs With | p-value N1-N2 vs With |
|--------------------|------------|------------|--|---------------------------|-----------------------|
| Up-regulated | | | | | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 22.5 | 0.025197485 |
| RC_W37778_f_at | 1002 | W37778 | ESTs, Weakly similar to envelope protein [H.sapiens] | -2.0 | 0.043013942 |
| AA248555_at | 164 | AA248555 | ESTs | -2.0 | 0.000824698 |
| RC_AA463693_at | 385 | AA463693 | ESTs, Weakly similar to SERINE/THREONINE-PROTEIN KINASE NEK3 [H.sapiens] | -2.0 | 0.002809026 |
| W76181_at | 1030 | W76181 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)5q31 | -2.0 | 0.008370263 |
| RC_AA171939_at | 106 | AA171939 | ESTs | -2.0 | 0.015796116 |
| U30999_at | 961 | U30999 | U30999 Homo sapiens MV3 melanoma Homo sapiens cDNA clone memd ... | -2.0 | 0.007070546 |
| RC_F03254_f_at | 527 | F03254 | synuclein, alpha (non A4 component of amyloid precursor)4q21 | -2.0 | 0.011479379 |
| RC_H26288_at | 567 | H26288 | ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | -2.0 | 0.000262324 |
| RC_AA007158_f_at | 4 | AA007158 | ESTs | -2.0 | 0.001870921 |
| RC_Z38785_at | 1109 | Z38785 | Homo sapiens clone 23940 mRNA sequence | -2.0 | 0.013437083 |
| RC_AA282247_at | 204 | AA282247 | ESTs | -2.0 | 0.000515617 |
| RC_T23935_s_at | 887 | T23935 | ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens] | -2.0 | 0.006493804 |
| RC_R59593_at | 848 | R59593 | ESTs | -2.0 | 0.014592934 |
| RC_AA446241_at | 345 | AA446241 | tropomyosin 2 (beta)9p13.2-p13.1 | -2.0 | 0.040680667 |
| RC_Z40556_at | 1116 | Z40556 | DJ222E13.1a.1 (C-terminal part of novel protein dJ222E13.1) (partial isoform 1) | -2.0 | 0.019444878 |
| RC_AA159025_at | 100 | AA159025 | ESTs, Highly similar to (defline not available 4680655) [H.sapiens] | -2.0 | 0.01375696 |
| RC_H03387_s_at | 546 | H03387 | estrogen-responsive B box protein17p11.2 | -2.0 | 0.036382844 |
| RC_H17333_at | 558 | H17333 | EST | -2.0 | 0.018111182 |
| RC_AA412722_s_at | 289 | AA412722 | putative cyclin G1 interacting protein7 | -2.0 | 0.006838915 |
| U65579_at | 979 | U65579 | NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)11q13 | -2.0 | 0.013707565 |
| RC_R88209_at | 860 | R88209 | ESTs | -2.0 | 0.040272012 |
| RC_Z38266_at | 1106 | Z38266 | Homo sapiens PAC clone DJ0777O23 from 7p14-p15 | -2.0 | 0.009414008 |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|-------------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| V01512_ma1_at | 993 | V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.0 | 0.001216643 | |
| RC_T90619_f_at | 926 | T90619 | actin, gamma 117q25 | 15.7 | 0.044124187 | |
| U20734_s_at | 952 | U20734 | jun B proto-oncogene19p13.2 | 14.3 | 0.004404553 | |
| U62015_at | 978 | U62015 | insulin-like growth factor binding protein 101p22-p31 | 13.8 | 0.000487216 | |
| AA374109_at | 241 | AA374109 | ESTs; Moderately similar to (define not available 5031506) [R.norvegicus] | 13.0 | 0.025911461 | |
| RC_T79768_at | 914 | T79768 | ESTs | 12.2 | 0.018940142 | |
| RC_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1)4q21 | 11.1 | 0.046025784 | |
| X52541_at | 1064 | X52541 | early growth response 15q31.1 | 9.7 | 0.003167537 | |
| RC_N66802_at | 767 | N66802 | early growth response 38p23-p21 | 9.7 | 0.026764792 | |
| RC_AA463726_s_at | 386 | AA463726 | JM27 proteinXp11.23 | 9.4 | 0.003409168 | |
| N40141_at | 743 | N40141 | JM27 proteinXp11.23 | 8.4 | 0.021768214 | |
| M34996_s_at | 685 | M34996 | major histocompatibility complex, class II, DQ alpha 16p21.3 | 7.7 | 0.015886207 | |
| RC_T67053_f_at | 909 | T67053 | immunoglobulin lambda gene cluster22q11.1-q11.2 | 7.4 | 0.000196865 | |
| RC_AA404957_at | 266 | AA404957 | ESTs, Highly similar to MATRIX GLA-PROTEIN PRECURSOR [H.sapiens] | 6.6 | 0.011451385 | |
| RC_H64493_f_at | 590 | H64493 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 6.5 | 0.002716347 | |
| RC_N47686_s_at | 744 | N47686 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group)18q11-q12 | 6.3 | 0.015568892 | |
| RC_W44760_s_at | 1006 | W44760 | frizzled-related protein2qter | 6.3 | 0.016891036 | |
| L19871_at | 642 | L19871 | activating transcription factor 3 | 6.2 | 0.007603286 | |
| M92934_at | 708 | M92934 | connective tissue growth factor6q23.1 | 6.1 | 0.001046931 | |
| M62831_at | 695 | M62831 | immediate early protein19 | 5.8 | 0.00753286 | |
| L22524_s_at | 643 | L22524 | matrix metalloproteinase 7 (matriasin, uterine)11q21-q22 | 5.8 | 0.048289798 | |
| J03507_at | 621 | J03507 | complement component 75p13 | 5.6 | 0.00240657 | |
| RC_AA236455_r_at | 153 | AA236455 | ESTs | 5.5 | 0.022653542 | |
| RC_AA450127_at | 359 | AA450127 | growth arrest and DNA-damage-inducible, beta19p13.3 | 5.5 | 0.023227588 | |
| RC_AA281345_f_at | 201 | AA281345 | immediate early protein19 | 5.4 | 0.003661068 | |
| RC_N30198_at | 733 | N30198 | ESTs | 5.3 | 0.005657756 | |
| AFFX-HSAC07/X00351_5_at | 1040 | X00351 | Human mRNA for beta-actin | 5.3 | 0.01547291 | |
| D83018_at | 513 | D83018 | nel (chicken)-like 212q13.11-q13.12 | 5.1 | 0.003774757 | |
| J04111_at | 624 | J04111 | Jun activation domain binding protein1p32-p31 | 5.0 | 0.000243067 | |
| X51345_at | 1062 | X51345 | jun B proto-oncogene19p13.2 | 5.0 | 0.017173421 | |
| RC_AA398903_at | 250 | AA398903 | ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | 4.9 | 0.014577818 | |
| RC_H17550_at | 559 | H17550 | ESTs | 4.7 | 0.012079391 | |
| S81914_at | 873 | S81914 | immediate early response 36p21.3 | 4.5 | 0.006218653 | |
| RC_AA250958_f_at | 167 | AA250958 | EST | 4.4 | 1.88343E-05 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1569988.1 |
|-------------------------|--|------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_AA446651_at | 346 | AA446651 | ESTs | 4.4 | 0.026022802 | |
| HG1872-HT1907_at | 674 | M28590 | Human (clone pcDG-79) MHC HLA-DG protein 41 mRNA, partial cds. | 4.3 | 0.008830524 | |
| RC_AA490667_at | 419 | AA490667 | ESTs | 4.3 | 0.048863016 | |
| RC_N67041_at | 768 | N67041 | ESTs | 4.1 | 0.009333688 | |
| V00563_at | 991 | V00563 | immunoglobulin mu14q32.33 | 4.1 | 0.004301939 | |
| X57809_s_at | 1069 | X57809 | immunoglobulin lambda gene cluster22q11.1-q11.2 | 4.1 | 0.025371658 | |
| R69417_at | 852 | R69417 | ESTs | 4.1 | 0.046373179 | |
| J00231_f_at | 617 | J00231 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 4.0 | 0.004766015 | |
| RC_AA402903_f_at | 263 | AA402903 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 3.9 | 0.000172905 | |
| U21128_at | 953 | U21128 | lumican12q21.3-q22 | 3.9 | 0.000708917 | |
| M12529_at | 655 | M12529 | apolipoprotein E19q13.2 | 3.7 | 0.026856247 | |
| RC_AA436616_at | 335 | AA436616 | ESTs | 3.7 | 0.020860083 | |
| U72649_at | 983 | U72649 | B-cell translocation gene 2 (pheochromacytoma cell-3)1q32 | 3.7 | 0.002487396 | |
| X03689_s_at | 1044 | X03689 | Human mRNA fragment for elongation factor TU (N-terminus) | 3.7 | 0.04821902 | |
| AFFX-HSAC07/X00351_5_at | 1040 | X00351 | Human mRNA for beta-actin | 3.6 | 0.029717275 | |
| RC_T62857_at | 903 | T62857 | ESTs | 3.6 | 0.002846539 | |
| Z74616_s_at | 1123 | Z74616 | collagen, type I, alpha 27q22.1 | 3.6 | 0.004328291 | |
| X06700_s_at | 1049 | X06700 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)2q31 | 3.6 | 0.010596098 | |
| RC_H86112_f_at | 600 | H86112 | KIAA0471 gene product1q24-q25 | 3.6 | 0.017013968 | |
| M57466_s_at | 690 | M57466 | major histocompatibility complex, class II, DP beta 16p21.3 | 3.5 | 0.005924671 | |
| RC_F09281_at | 533 | F09281 | ESTs | 3.5 | 0.006841731 | |
| RC_R51831_at | 843 | R51831 | ESTs | 3.4 | 0.000941423 | |
| RC_H21814_f_at | 563 | H21814 | immunoglobulin lambda gene cluster22q11.1-q11.2 | 3.4 | 0.009767098 | |
| RC_W86513_at | 1033 | W86513 | ESTs | 3.4 | 0.003776481 | |
| RC_H40424_s_at | 572 | H40424 | EST | 3.4 | 0.016283906 | |
| X57025_at | 1066 | X57025 | insulin-like growth factor 1 (somatomedin C)12q22 q23 | 3.3 | 0.040489253 | |
| RC_AA044219_at | 29 | AA044219 | BK984G1.1 (PUTATIVE C-terminal end of a novel protein with Collagen triple helix repeats) | 3.3 | 0.001761114 | |
| RC_AA028092_s_at | 17 | AA028092 | transcription factor 216pter-qter | 3.3 | 0.003405482 | |
| RC_AA446661_at | 347 | AA446661 | ESTs | 3.3 | 0.041188995 | |
| RC_D80063_f_at | 505 | D80063 | ESTs | 3.3 | 0.049585142 | |
| M92843_s_at | 707 | M92843 | zinc finger protein homologous to Zfp-36 in mouse19q13.1 | 3.3 | 0.006174082 | |
| M34516_r_at | 684 | M34516 | immunoglobulin lambda-like polypeptide 322q11.2 | 3.2 | 0.02344053 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|---------------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| M87789_s_at | 704 | M87789 | immunoglobulin gamma 3 (Gm marker)14q32.33 | 3.2 | 0.004534646 | |
| N75870_s_at | 780 | N75870 | dual specificity phosphatase 15q34 | 3.2 | 0.000157434 | |
| RC_AA609309_at | 442 | AA609309 | ESTs, Moderately similar to !!!! ALU SUBFAMILY | 3.1 | 0.03780658 | |
| S59049_at | 870 | S59049 | SB2 WARNING ENTRY !!!! [H.sapiens] regulator of G-protein signalling 11q31 | 3.0 | 0.002419303 | |
| AFFX-HUMGAPDH/M33197_5_at | 679 | M33197 | Human GAPDH | 3.0 | 0.034538288 | |
| RC_D51060_s_at | 495 | D51060 | Jun activation domain binding protein1p32-p31 | 3.0 | 0.022390037 | |
| RC_T23468_at | 884 | T23468 | ESTs | 2.9 | 0.001634616 | |
| U30521_at | 960 | U30521 | P311 protein | 2.9 | 0.009484198 | |
| Z48501_s_at | 1121 | Z48501 | poly(A)-binding protein-like 13q22-q25 | 2.9 | 0.026396977 | |
| W73859_at | 1028 | W73859 | transcription factor 216pter-qter | 2.9 | 0.037326183 | |
| AA093923_at | 63 | AA093923 | tissue inhibitor of metalloproteinase 217q25 | 2.8 | 0.041564022 | |
| RC_AA236476_at | 154 | AA236476 | ESTs, Weakly similar to (defline not available 4507549) [H.sapiens] | 2.7 | 0.038305276 | |
| U10550_at | 944 | U10550 | GTP-binding protein overexpressed in skeletal muscle8q13-q21 | 2.7 | 0.040657885 | |
| RC_N24902_at | 727 | N24902 | E1B-55kDa-associated protein 5 | 2.7 | 0.03810507 | |
| RC_AA056121_at | 46 | AA056121 | ESTs | 2.7 | 0.024285705 | |
| RC_H98835_at | 611 | H98835 | ESTs | 2.7 | 0.019901442 | |
| K02405_f_at | 629 | K02405 | Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds | 2.7 | 0.00138806 | |
| U90552_s_at | 988 | U90552 | butyrophilin, subfamily 3, member A16p23 | 2.7 | 3.91186E-05 | |
| RC_N59831_at | 759 | N59831 | ESTs | 2.7 | 0.04543669 | |
| L33799_at | 645 | L33799 | procollagen C-endopeptidase enhancer7q22 | 2.7 | 0.010879277 | |
| RC_N59532_s_at | 758 | N59532 | aminomethyltransferase (glycine cleavage system protein T)3p21.2-p21.1 | 2.6 | 0.025712285 | |
| D13628_at | 476 | D13628 | angiopoietin 18q22.3-q23 | 2.6 | 0.027204836 | |
| AA156897_s_at | 97 | AA156897 | Homo sapiens mRNA; cDNA DKFZp564I1922 (from clone DKFZp564I1922) | 2.6 | 0.001580022 | |
| RC_N67876_s_at | 773 | N67876 | insulin-like growth factor 1 (somatomedin C)12q22 q23 | 2.6 | 0.03992641 | |
| M73720_at | 702 | M73720 | carboxypeptidase A3 (mast cell)3q21-q25 | 2.6 | 0.023298997 | |
| H49440_at | 578 | H49440 | nudix (nucleoside diphosphate linked moiety X)- type motif 36p21.2 | 2.6 | 0.002498701 | |
| RC_AA250850_at | 166 | AA250850 | adrenergic, beta, receptor kinase 222q11 | 2.5 | 0.041156086 | |
| RC_T49061_at | 894 | T49061 | ESTs | 2.5 | 0.00934004 | |
| W28214_at | 996 | W28214 | ESTs | 2.5 | 0.037677921 | |
| RC_H44631_s_at | 573 | H44631 | immediate early protein19 | 2.5 | 0.0423037 | |
| D28137_at | 484 | D28137 | bone marrow stromal cell antigen 219p13.2 | 2.5 | 0.026212334 | |
| RC_AA609027_at | 441 | AA609027 | ESTs | 2.5 | 0.038550623 | |
| RC_AA257093_r_at | 178 | AA257093 | T-cell receptor, beta cluster7q35 | 2.4 | 0.002653232 | |
| RC_F13763_at | 542 | F13763 | ESTs | 2.4 | 0.016949277 | |
| RC_H08548_s_at | 550 | H08548 | ATP citrate lyase17q12-q21 | 2.4 | 0.036998522 | |
| RC_AA436618_at | 336 | AA436618 | ESTs | 2.4 | 0.001789907 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|-------------------------|--|------------|--|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID NO: | Genbank ID | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_W45664_s_at | 1008 | W45664 | 5' nucleotidase (CD73)6q14-q21 | 2.4 | 0.001762727 | |
| AA082546_at | 54 | AA082546 | ESTs | 2.4 | 0.021791878 | |
| D10522_at | 471 | D10522 | myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)6q22.2 | 2.4 | 0.017333686 | |
| RC_AA411860_at | 280 | AA411860 | ESTs, Highly similar to (define not available 4929723) [H.sapiens] | 2.4 | 0.02766922 | |
| AB002340_at | 461 | AB002340 | KIAA0342 gene product | 2.3 | 0.003238699 | |
| U53445_at | 972 | U53445 | downregulated in ovarian cancer 13 | 2.3 | 0.009361652 | |
| AA091278_at | 60 | AA091278 | ESTs | 2.3 | 0.046253689 | |
| RC_AA486072_i_at | 410 | AA486072 | small inducible cytokine A5 (RANTES)17q11.2-q12 | 2.3 | 0.012816473 | |
| RC_T53590_s_at | 899 | T53590 | cytochrome P450, subfamily XIA (cholesterol side chain cleavage)15q23-q24 | 2.3 | 4.29636E-05 | |
| RC_N91971_f_at | 791 | N91971 | retinol-binding protein 1, cellular3q23 | 2.3 | 0.025171598 | |
| RC_AA043777_at | 28 | AA043777 | ESTs | 2.3 | 0.004490188 | |
| RC_H54764_at | 580 | H54764 | EST, Weakly similar to X-linked retinopathy protein {C-terminal, clone XEH.8c} [H.sapiens] | 2.3 | 0.036980431 | |
| RC_AA443923_at | 344 | AA443923 | ESTs | 2.3 | 0.025833241 | |
| U60975_at | 977 | U60975 | Homo sapiens gp250 precursor, mRNA, complete cds. | 2.3 | 0.041238204 | |
| M34516_at | 684 | M34516 | immunoglobulin lambda-like polypeptide 322q11.2 | 2.3 | 0.041388637 | |
| RC_N36001_at | 740 | N36001 | ESTs, Weakly similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens] | 2.2 | 0.000449076 | |
| AF010193_at | 464 | AF010193 | MAD (mothers against decapentaplegic, Drosophila) homolog 718 | 2.2 | 0.005397771 | |
| AFFX-HSAC07/X00351_5_at | 1040 | X00351 | Human mRNA for beta-actin | 2.2 | 0.037852217 | |
| RC_AA158262_s_at | 99 | AA158262 | calpastatin5q14-q22 | 2.2 | 0.006648962 | |
| RC_AA156565_at | 96 | AA156565 | 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like 122q12 | 2.2 | 0.020901922 | |
| Z11793_at | 1104 | Z11793 | selenoprotein P, plasma, 15q31 | 2.2 | 0.00118281 | |
| RC_D80059_s_at | 504 | D80059 | ESTs | 2.2 | 0.033534432 | |
| RC_AA450324_at | 360 | AA450324 | ESTs | 2.2 | 0.024832006 | |
| RC_N39415_at | 742 | N39415 | osteoglycin (osteoinductive factor) | 2.2 | 0.032001116 | |
| RC_T23622_at | 886 | T23622 | ESTs | 2.2 | 0.040417825 | |
| RC_AA599365_at | 434 | AA599365 | decorin12q23 | 2.2 | 0.011325181 | |
| X62320_at | 1073 | X62320 | granulin17 | 2.2 | 0.043043858 | |
| RC_R85291_at | 859 | R85291 | ESTs | 2.2 | 0.004987693 | |
| M11313_s_at | 654 | M11313 | alpha-2-macroglobulin12p13.3-p12.3 | 2.2 | 0.011545737 | |
| AA047151_at | 37 | AA047151 | ESTs | 2.2 | 0.033987576 | |
| RC_AA205724_at | 123 | AA205724 | ESTs | 2.2 | 0.004569368 | |
| RC_AA086264_i_at | 59 | AA086264 | ESTs, Highly similar to (define not available 4191348) [H.sapiens] | 2.2 | 0.020637423 | |
| RC_R42424_at | 832 | R42424 | ESTs | 2.2 | 0.033603417 | |
| RC_AA347359_s_at | 233 | AA347359 | lysozyme (renal amyloidosis)12 | 2.1 | 0.028764499 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|--------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| AA092716_at | 62 | AA092716 | HLA-B associated transcript-36p21.3 | 2.1 | 0.031717351 | |
| RC_R42241_at | 830 | R42241 | ESTs | 2.1 | 0.008013968 | |
| RC_N57577_at | 756 | N57577 | KIAA0663 gene product | 2.1 | 0.032028875 | |
| RC_W67577_s_at | 1022 | W67577 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)5q32 | 2.1 | 0.002072118 | |
| C02016_at | 466 | C02016 | KIAA0447 gene product | 2.1 | 0.002399894 | |
| RC_AA256268_at | 175 | AA256268 | ESTs | 2.1 | 0.0269568 | |
| RC_T96171_at | 930 | T96171 | EST | 2.1 | 0.012219229 | |
| X72841_at | 1083 | X72841 | retinoblastoma-binding protein 7 | 2.1 | 0.033774692 | |
| RC_R45698_at | 839 | R45698 | ESTs | 2.1 | 0.049975895 | |
| RC_N22006_s_at | 719 | N22006 | EST | 2.1 | 0.011131338 | |
| RC_N69222_at | 777 | N69222 | ESTs | 2.1 | 0.022256915 | |
| RC_H97538_at | 607 | H97538 | ESTs | 2.0 | 0.03795259 | |
| RC_AA039935_at | 23 | AA039935 | dynein light chain, outer arm 422q12.3-q13.2 | 2.0 | 0.011488766 | |
| RC_AA084138_at | 55 | AA084138 | ESTs | 2.0 | 0.011124432 | |
| AB002379_at | 462 | AB002379 | KIAA0381 protein | 2.0 | 0.000530413 | |
| RC_AA460651_at | 379 | AA460651 | heterogeneous nuclear protein similar to rat helix destabilizing protein10 | 2.0 | 0.027697892 | |
| RC_W02204_at | 994 | W02204 | solute carrier family 24 (sodium/potassium/calcium exchanger), member 115q22 | 2.0 | 0.00115779 | |
| Y08614_at | 1101 | Y08614 | exportin 1 (CRM1, yeast, homolog)2p16 | 2.0 | 0.035368368 | |
| D31134_at | 488 | D31134 | KIAA1075 protein | 2.0 | 0.021196526 | |
| M94880_f_at | 711 | M94880 | major histocompatibility complex, class I, A6p21.3 | 2.0 | 0.025382167 | |
| J03040_at | 619 | J03040 | secreted protein, acidic, cysteine-rich (osteonectin)5q31.3-q32 | 2.0 | 0.035472553 | |
| RC_N68350_at | 775 | N68350 | ESTs | 2.0 | 0.042917893 | |
| RC_H48793_at | 577 | H48793 | EST | 2.0 | 0.00296551 | |
| HG3543-HT3739_at | 675 | M29645 | insulin-like growth factor 2 (somatomedin A)11p15.5 | 2.0 | 0.019712374 | |
| RC_W33172_at | 999 | W33172 | ESTs, Weakly similar to ORF2 [M.musculus] | 2.0 | 0.006454106 | |
| RC_R08850_at | 806 | R08850 | ESTs | 2.0 | 0.011364766 | |
| W52638_at | 1014 | W52638 | ESTs | 2.0 | 0.010612401 | |
| M19045_f_at | 662 | M19045 | lysozyme (renal amyloidosis)12 | 2.0 | 0.004561974 | |
| RC_AA312946_s_at | 228 | AA312946 | ESTs | 2.0 | 0.020272205 | |
| RC_AA235310_at | 148 | AA235310 | ESTs | 2.0 | 0.011954937 | |
| X03100_cds2_at | 1043 | X03100 | Human mRNA for SB classII histocompatibility antigen alpha-chain | 2.0 | 0.002404541 | |
| RC_T16282_f_at | 881 | T16282 | wee1+ (S. pombe) homolog11p15.3-p15.1 | 2.0 | 0.031472155 | |
| RC_H66642_f_at | 591 | H66642 | ESTs, Moderately similar to !!!! ALU SUBFAMILY | 2.0 | 0.02460529 | |
| RC_AA342337_at | 231 | AA342337 | SQ WARNING ENTRY !!!! [H.sapiens] ESTs, Moderately similar to !!!! ALU SUBFAMILY | -23.7 | 3.26344E-05 | |

SQ WARNING ENTRY !!!! [H.sapiens]

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
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| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_AA398908_at | 251 | AA398908 | Human Chromosome 16 BAC clone CIT987SK-A-61E3 | -21.7 | 0.040053626 | |
| RC_H15143_s_at | 554 | H15143 | Human clone 23575 mRNA, partial cds | -13.8 | 0.028261625 | |
| RC_N80129_i_at | 785 | N80129 | metallothionein 1L16q13 | -12.6 | 0.002146038 | |
| RC_AA465394_at | 390 | AA465394 | ESTs | -12.6 | 0.004961162 | |
| RC_AA236545_at | 156 | AA236545 | ESTs | -12.5 | 0.034938167 | |
| RC_W42778_at | 1004 | W42778 | Homo sapiens clone 24636 mRNA sequence | -12.3 | 0.010449419 | |
| RC_T40895_at | 892 | T40895 | ESTs | -12.0 | 0.01968535 | |
| RC_H94475_s_at | 605 | H94475 | alpha-2-plasmin inhibitor17pter-p12 | -11.7 | 0.012919819 | |
| RC_R71792_s_at | 855 | R71792 | ESTs, Moderately similar to FAT-SPECIFIC PROTEIN FSP27 [M.musculus] | -10.4 | 0.002540356 | |
| RC_AA609006_at | 440 | AA609006 | ESTs | -7.5 | 0.013902978 | |
| RC_AA026641_s_at | 16 | AA026641 | secretory leukocyte protease inhibitor (antileukoproteinase) | -7.0 | 0.01850877 | |
| X65614_at | 1076 | X65614 | S100 calcium-binding protein P4p16 | -6.7 | 0.005634308 | |
| X93036_at | 1093 | X93036 | phospholemmann-like, expressed in breast tumors, 8kD | -6.6 | 0.005278275 | |
| RC_T94447_s_at | 928 | T94447 | ESTs, Moderately similar to (defline not available 4335935) [M.musculus] | -5.7 | 0.006891909 | |
| RC_AA405488_at | 268 | AA405488 | ESTs | -5.5 | 0.00023986 | |
| RC_T73433_s_at | 912 | T73433 | angiotensinogen1q41-qter | -5.5 | 0.009418205 | |
| M99487_at | 716 | M99487 | folate hydrolase (prostate-specific membrane antigen) 111p11.2 | -5.3 | 0.008067789 | |
| RC_W88568_at | 1035 | W88568 | glycogenin 2Xp22.3 | -5.1 | 0.024739084 | |
| RC_AA460914_at | 380 | AA460914 | ESTs | -5.0 | 0.024385552 | |
| X57129_at | 1067 | X57129 | H1 histone family, member 26p21.3 | -4.8 | 0.006322499 | |
| RC_Z41642_at | 1119 | Z41642 | ESTs | -4.7 | 0.009525521 | |
| RC_R46074_at | 840 | R46074 | transforming, acidic coiled-coil containing protein 210q26 | -4.7 | 0.001327844 | |
| J03910_rna1_at | 622 | J03910 | metallothionein 1G16q13 | -4.6 | 0.004574277 | |
| RC_AA350265_at | 237 | AA350265 | histone deacetylase A | -4.5 | 0.002897414 | |
| AA165312_at | 103 | AA165312 | ESTs | -4.2 | 0.005487803 | |
| RC_AA419011_at | 296 | AA419011 | Homo sapiens mRNA; cDNA DKFZp586D0823 (from clone DKFZp586D0823) | -4.0 | 0.019079557 | |
| RC_N92502_s_at | 794 | N92502 | ESTs, Moderately similar to HERV-E integrase [H.sapiens] | -4.0 | 0.030144039 | |
| RC_F03969_at | 528 | F03969 | ESTs, Weakly similar to tumorous imaginal discs protein Tid56 homolog [H.sapiens] | -4.0 | 0.017024613 | |
| X76717_at | 1087 | X76717 | metallothionein 1L16q13 | -3.9 | 0.001145402 | |
| RC_AA416762_s_at | 291 | AA416762 | nuclear receptor subfamily 1, group H, member 219q13.3-19q13.3 | -3.8 | 0.011735303 | |
| RC_AA053424_at | 40 | AA053424 | ESTs, Weakly similar to mucin Muc3 [R.norvegicus] | -3.8 | 0.009737433 | |
| X64177_f_at | 1075 | X64177 | metallothionein 1H16q13 | -3.7 | 0.003297195 | |
| RC_N32748_at | 736 | N32748 | ESTs | -3.6 | 0.021454174 | |
| RC_AA416685_at | 290 | AA416685 | UNC13 (C. elegans)-like9p11-p12 | -3.6 | 0.016338392 | |
| RC_AA505136_at | 426 | AA505136 | ESTs | -3.5 | 0.007200396 | |
| RC_AA165313_at | 104 | AA165313 | ESTs | -3.5 | 0.037649191 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|--------------------|--|----------------|--|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_F02245_at | 522 | F02245 | monoamine oxidase AXp11.4-p11.3 | -3.4 | 0.005486135 | |
| RC_AA004699_at | 1 | AA004699 | putative translation initiation factor | -3.4 | 0.00057505 | |
| RC_AA599331_at | 433 | AA599331 | ESTs | -3.4 | 0.01136457 | |
| RC_N26904_at | 731 | N26904 | ESTs, Weakly similar to FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens] | -3.3 | 0.045410608 | |
| RC_AA070752_s_at | 51 | AA070752 | insulin receptor substrate 12q36 | -3.3 | 0.028433761 | |
| RC_AA599522_f_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | -3.2 | 0.005311305 | |
| RC_N94303_at | 797 | N94303 | ESTs | -3.1 | 0.000160723 | |
| RC_F10078_at | 538 | F10078 | ESTs | -3.1 | 0.022464594 | |
| RC_AA447537_at | 350 | AA447537 | ESTs, Moderately similar to (defline not available 5360237) [M.musculus] | -3.1 | 0.007323728 | |
| L77701_at | 651 | L77701 | human homolog of yeast mitochondrial copper recruitment gene | -3.0 | 0.001489928 | |
| RC_H27675_at | 569 | H27675 | ESTs | -3.0 | 0.016160504 | |
| V00594_at | 992 | V00594 | metallothionein 2A16q13 | -2.9 | 0.001495259 | |
| U52969_at | 970 | U52969 | Purkinje cell protein 421q22.2-q22.3 | -2.9 | 6.3447E-05 | |
| RC_R42607_at | 834 | R42607 | ESTs | -2.8 | 0.008960052 | |
| RC_AA451836_at | 362 | AA451836 | ESTs | -2.7 | 0.008401586 | |
| RC_F04492_at | 531 | F04492 | ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | -2.7 | 0.001443051 | |
| RC_H77597_f_at | 594 | H77597 | metallothionein 1H16q13 | -2.7 | 0.00332868 | |
| RC_AA430388_at | 321 | AA430388 | ESTs, Moderately similar to !!!! ALU SUBFAMILY | -2.7 | 0.000114004 | |
| RC_T90190_s_at | 925 | T90190 | SQ WARNING ENTRY !!!! [H.sapiens] | -2.7 | 0.030242714 | |
| RC_H16171_f_at | 555 | H16171 | H1 histone family, member 26p21.3 | -2.7 | 0.023414443 | |
| RC_AA022886_at | 14 | AA022886 | clef lip and palate associated transmembrane protein 119q13.2-q13.3 | -2.7 | 0.00489294 | |
| RC_R28370_at | 815 | R28370 | ESTs, Weakly similar to phosphatidylinositol transfer protein [H.sapiens] | -2.7 | 0.003724547 | |
| RC_AA261907_at | 182 | AA261907 | ESTs, Weakly similar to (defline not available 3874144) [C.elegans] | -2.6 | 0.043689441 | |
| RC_W37778_f_at | 1002 | W37778 | ESTs, Weakly similar to envelope protein [H.sapiens] | -2.6 | 0.030756837 | |
| RC_T98019_at | 932 | T98019 | EST, Highly similar to PEREGRIN [H.sapiens] | -2.5 | 0.035566681 | |
| RC_N33927_s_at | 737 | N33927 | H2B histone family, member B6p21.3 | -2.5 | 0.013093926 | |
| RC_R40431_at | 828 | R40431 | Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016) | -2.5 | 0.004235538 | |
| RC_AA133756_at | 78 | AA133756 | Rho-associated, coiled-coil containing protein kinase 22p24 | -2.5 | 0.012389163 | |
| RC_AA152200_s_at | 92 | AA152200 | ESTs | -2.5 | 0.004366137 | |
| W63793_at | 1020 | W63793 | S-adenosylmethionine decarboxylase 16q21-q22 | -2.5 | 0.005714247 | |
| RC_AA410298_at | 274 | AA410298 | ESTs | -2.5 | 0.018744617 | |
| X99728_at | 1098 | X99728 | H.sapiens NDUFV3 gene, exon 3 | -2.5 | 0.004580383 | |
| RC_W78127_at | 1031 | W78127 | ESTs, Weakly similar to KIAA0425 [H.sapiens] | -2.5 | 0.001240164 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|--------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_R96924_s_at | 866 | R96924 | ESTs | -2.5 | 0.006515911 | |
| RC_H16768_at | 557 | H16768 | ESTs | -2.5 | 0.005669237 | |
| X76180_at | 1086 | X76180 | sodium channel, nonvoltage-gated 1 alpha12p13 | -2.5 | 0.007625025 | |
| RC_AA432162_at | 324 | AA432162 | Homo sapiens mRNA; cDNA DKFZp586B2022 (from clone DKFZp586B2022) | -2.4 | 0.010199113 | |
| RC_H88798_at | 602 | H88798 | ESTs | -2.4 | 0.000783143 | |
| RC_AA609312_at | 443 | AA609312 | ESTs | -2.4 | 0.016243321 | |
| RC_AA131919_at | 75 | AA131919 | putative type II membrane protein | -2.4 | 0.000264791 | |
| RC_N80129_f_at | 785 | N80129 | metallothionein 1L16q13 | -2.4 | 0.002297016 | |
| RC_AA182030_at | 110 | AA182030 | ESTs | -2.4 | 0.041632378 | |
| W70167_at | 1025 | W70167 | ESTs | -2.4 | 0.00395969 | |
| RC_AA599522_r_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | -2.4 | 0.004347078 | |
| RC_N52254_s_at | 749 | N52254 | SH3-binding domain glutamic acid-rich protein21q22.3 | -2.4 | 0.011171389 | |
| RC_N95495_at | 799 | N95495 | small inducible cytokine A5 (RANTES)17q11.2-q12 | -2.4 | 0.002430242 | |
| RC_T68873_f_at | 911 | T68873 | metallothionein 1L16q13 | -2.4 | 0.00320019 | |
| AA429539_f_at | 318 | AA429539 | ESTs | -2.4 | 0.020751882 | |
| RC_AA435769_s_at | 330 | AA435769 | ESTs | -2.4 | 0.009832353 | |
| RC_AA029356_at | 18 | AA029356 | ESTs | -2.3 | 0.007208722 | |
| AA316686_s_at | 229 | AA316686 | ESTs, Highly similar to huntingtin interacting protein HYPK [H.sapiens] | -2.3 | 0.000225753 | |
| RC_H02308_at | 545 | H02308 | ESTs | -2.3 | 0.041776289 | |
| RC_AA258476_at | 179 | AA258476 | Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) | -2.3 | 0.02070961 | |
| X06956_at | 1051 | X06956 | tubulin, alpha 1 (testis specific)2q | -2.3 | 0.003656874 | |
| RC_H99694_at | 614 | H99694 | ESTs | -2.3 | 0.013645335 | |
| RC_AA479044_s_at | 402 | AA479044 | ESTs, Weakly similar to PROGASTRICSIN PRECURSOR [H.sapiens] | -2.3 | 0.047032301 | |
| RC_AA436861_at | 340 | AA436861 | ESTs | -2.3 | 0.001794201 | |
| M24069_at | 672 | M24069 | cold shock domain protein A12p13.1 | -2.3 | 0.014123514 | |
| RC_AA410311_at | 275 | AA410311 | ESTs | -2.3 | 0.045227011 | |
| W52858_at | 1015 | W52858 | Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522) | -2.3 | 0.002276405 | |
| RC_W38197_at | | W38197 | EST | -2.3 | 1.96016E-05 | |
| J00073_at | 615 | J00073 | actin, alpha, cardiac muscle15q11-qter | -2.3 | 0.018476889 | |
| RC_D51069_f_at | 496 | D51069 | melanoma adhesion molecule | -2.3 | 0.042693395 | |
| RC_AA504805_s_at | 424 | AA504805 | interferon stimulated gene (20kD)15q26 | -2.3 | 0.008805886 | |
| RC_F03254_f_at | 527 | F03254 | synuclein, alpha (non A4 component of amyloid precursor)4q21 | -2.3 | 0.003668915 | |
| M35252_at | 686 | M35252 | transmembrane 4 superfamily member 3 | -2.3 | 0.028083185 | |
| RC_AA040731_at | 25 | AA040731 | ESTs | -2.2 | 0.028924808 | |
| RC_AA496247_at | 422 | AA496247 | ESTs | -2.2 | 0.013336314 | |
| X59766_at | 1071 | X59766 | alpha-2-glycoprotein 1, zinc7 | -2.2 | 0.002003511 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|--------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| RC_R84421_at | 857 | R84421 | eukaryotic translation elongation factor 1 alpha 16q14 | -2.2 | 0.016333706 | |
| AA328993_s_at | 230 | AA328993 | ESTs | -2.2 | 0.004438605 | |
| RC_R44535_f_at | 836 | R44535 | endonuclease G9q34.1 | -2.2 | 0.014319616 | |
| U41518_at | 964 | U41518 | aquaporin 1 (channel-forming integral protein, 28kD)7p14 | -2.2 | 0.009447457 | |
| RC_W33179_at | 1000 | W33179 | testis-specific kinase 21p32 | -2.2 | 0.001104272 | |
| RC_H58873_s_at | 583 | H58873 | solute carrier family 2 (facilitated glucose transporter), member 11p35-p31.3 | -2.2 | 0.000238641 | |
| RC_R31679_s_at | 816 | R31679 | ESTs | -2.2 | 0.01000414 | |
| RC_AA189083_at | 114 | AA189083 | ESTs, Highly similar to (defline not available 4589468) [M.musculus] | -2.2 | 0.002468046 | |
| RC_AA251769_at | 168 | AA251769 | ESTs, Weakly similar to Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [H.sapiens] | -2.2 | 0.010819016 | |
| RC_W70131_at | 1024 | W70131 | ESTs | -2.2 | 0.02955725 | |
| RC_R09379_at | 807 | R09379 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13 | -2.2 | 0.009730513 | |
| RC_AA621695_at | 458 | AA621695 | ESTs | -2.1 | 0.001994051 | |
| RC_H18947_at | 561 | H18947 | ESTs | -2.1 | 0.027246274 | |
| RC_AA219552_s_at | 134 | AA219552 | ESTs | -2.1 | 0.046510941 | |
| RC_N22620_at | 722 | N22620 | ESTs | -2.1 | 0.013527392 | |
| RC_R02003_r_at | 804 | R02003 | ESTs, Weakly similar to cappuccino [D.melanogaster] | -2.1 | 0.010597095 | |
| RC_AA405559_at | 270 | AA405559 | ESTs | -2.1 | 0.009305601 | |
| RC_AA463693_at | 385 | AA463693 | ESTs, Weakly similar to SERINE/THREONINE-PROTEIN KINASE NEK3 [H.sapiens] | -2.1 | 0.004156996 | |
| RC_AA481407_at | 405 | AA481407 | ESTs | -2.1 | 0.002741696 | |
| M11119_at | 653 | M11119 | Human endogenous retrovirus envelope region mRNA (PL1) | -2.1 | 0.003718876 | |
| RC_AA159025_at | 100 | AA159025 | ESTs, Highly similar to (defline not available 4680655) [H.sapiens] | -2.1 | 0.011127532 | |
| RC_AA411981_at | 283 | AA411981 | ESTs, Weakly similar to putative seven pass transmembrane protein [H.sapiens] | -2.1 | 0.044294612 | |
| RC_W57931_at | 1017 | W57931 | ESTs, Moderately similar to CATHEPSIN D PRECURSOR [H.sapiens] | -2.1 | 0.000755739 | |
| X66899_at | 1081 | X66899 | Ewing sarcoma breakpoint region 122q12 | -2.1 | 0.002068901 | |
| RC_R49327_at | 842 | R49327 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 212q13 | -2.1 | 0.030928835 | |
| RC_AA609645_at | 445 | AA609645 | eukaryotic translation initiation factor 4 gamma, 13q27-qter | -2.1 | 0.04955957 | |
| RC_AA434108_at | 327 | AA434108 | Homo sapiens heat shock protein hsp40-3 mRNA, complete cds | -2.1 | 0.034468752 | |
| X17567_s_at | 1061 | X17567 | small nuclear ribonucleoprotein polypeptides B and B120 | -2.1 | 0.014475221 | |

| Table 2 | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | 1669988.1 |
|--------------------|--|----------------|---|-----------------------------|-------------------------|-----------|
| Affymetrix element | SEQ ID | Genbank ID NO: | Genbank Name | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | 16.5 | 8.98673E-05 | |
| J04164_at | 626 | J04164 | interferon-induced protein 17 | -2.1 | 0.023410352 | |
| RC_AA135929_s_at | 80. | AA135929 | ESTs, Highly similar to (define not available 4103057) [M.musculus] | -2.1 | 0.003009065 | |
| L04270_at | 634 | L04270 | lymphotoxin beta receptor (TNFR superfamily, member 312p13 | -2.1 | 0.006776988 | |
| RC_H99035_at | 612 | H99035 | ESTs | -2.1 | 0.001053884 | |
| M64673_at | 698 | M64673 | heat shock transcription factor 1 | -2.1 | 0.004283001 | |
| X85785_ma1_at | 1091 | X85785 | Duffy blood group1q21-q22 | -2.1 | 0.00657464 | |
| M68864_at | 700 | M68864 | Human ORF mRNA, complete cds | -2.1 | 0.010185833 | |
| D50928_at | 494 | D50928 | KIAA0138 gene product | -2.1 | 0.002283064 | |
| RC_AA282247_at | 204 | AA282247 | ESTs | -2.0 | 0.007970044 | |
| RC_R00144_at | 801 | R00144 | ESTs | -2.0 | 0.006939854 | |
| RC_AA485965_at | 409 | AA485965 | ESTs, Highly similar to (define not available 4336766) [H.sapiens] | -2.0 | 0.000405037 | |
| S45630_at | 869 | S45630 | crystallin, alpha B11q22.3-q23.1 | -2.0 | 0.006157273 | |
| RC_T89703_at | 923 | T89703 | ESTs, Highly similar to (define not available 4455129) [H.sapiens] | -2.0 | 0.000286616 | |
| RC_Z38785_at | 1109 | Z38785 | Homo sapiens clone 23940 mRNA sequence | -2.0 | 0.00706437 | |
| X85373_at | 1090 | X85373 | small nuclear ribonucleoprotein polypeptide G | -2.0 | 6.93881E-05 | |
| RC_F04816_at | 532 | F04816 | ESTs | -2.0 | 0.005353184 | |
| RC_AA043349_at | 27 | AA043349 | ESTs | -2.0 | 0.01749596 | |
| RC_H84761_s_at | 599 | H84761 | glutathione peroxidase 13p21.3 | -2.0 | 0.000116621 | |
| M34338_s_at | 683 | M34338 | spermidine synthase1p36-p22 | -2.0 | 0.008566137 | |
| L13698_at | 638 | L13698 | growth arrest-specific 19q21.3-q22.1 | -2.0 | 0.016504513 | |
| RC_N75960_at | 781 | N75960 | ESTs | -2.0 | 0.024082428 | |
| D45370_at | 491 | D45370 | adipose specific 210 | -2.0 | 0.034362163 | |
| RC_AA401965_at | 258 | AA401965 | tumor suppressor deleted in oral cancer-related 111q13 | -2.0 | 0.011190087 | |
| RC_F09315_at | 534 | F09315 | discs, large (Drosophila) homolog 510q23 | -2.0 | 0.020753036 | |
| RC_AA025370_at | 15 | AA025370 | KIAA0872 protein | -2.0 | 0.026565555 | |
| RC_H52835_at | 579 | H52835 | phytanoyl-CoA hydroxylase (Refsum disease)10pter-p11.2 | -2.0 | 0.015021251 | |
| RC_H99648_s_at | 613 | H99648 | DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis5q22-q23 | -2.0 | 0.012115852 | |
| RC_AA430074_at | 320 | AA430074 | ESTs | -2.0 | 0.002355049 | |
| RC_AA598939_at | 428 | AA598939 | ESTs | -2.0 | 0.011383872 | |
| AA455001_s_at | 368 | AA455001 | ESTs | -2.0 | 0.000176199 | |
| RC_F09684_at | 535 | F09684 | ESTs | -2.0 | 0.002741682 | |
| D42073_at | 490 | D42073 | reticulocalbin 1, EF-hand calcium binding domain11p13 | -2.0 | 0.012881688 | |
| RC_AA598695_at | 427 | AA598695 | ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] | -2.0 | 4.77268E-06 | |
| D23662_at | 481 | D23662 | neural precursor cell expressed, developmentally down-regulated 8 | -2.0 | 0.003156141 | |
| RC_AA431470_at | 323 | AA431470 | protein kinase (cAMP-dependent, catalytic) inhibitor gamma20q | -2.0 | 0.038692982 | |
| RC_AA399273_at | 253 | AA399273 | ESTs | -2.0 | 0.029403118 | |
| RC_AA142858_at | 82 | AA142858 | ESTs | -2.0 | 0.00197166 | |

| Affymetrix element | Normal1-Normal2 vs BPH-Cancer (Up-regulated) | | | | | Fold-Change N1-N2 vs Cancer | p-value N1-N2 vs Cancer | 1669988.1 |
|--------------------|--|------------|--|--|--|-----------------------------------|-------------------------------|-----------|
| | SEQ ID NO: | Genbank ID | Genbank Name | | | | | |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B19q13.3 | | | 18.8 | 0.03580379 | |
| RC_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog14q24.3 | | | 16.5 | 8.98673E-05 | |
| RC_Z40715_at | 1117 | Z40715 | Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201) | | | -2.0 | 0.017206338 | |
| RC_AA490341_s_at | 417 | AA490341 | ESTs | | | -2.0 | 0.004570941 | |
| RC_N67815_f_at | 772 | N67815 | ESTs, Weakly similar to (define not available 4680655) [H.sapiens] | | | -2.0 | 0.002996692 | |
| RC_N53359_at | 750 | N53359 | ESTs | | | -2.0 | 0.034916164 | |

| TABLE 3 Affymetrix element | Normal vs. BPH W/Symptoms (Up-regulated) | | | 1678621.1 | Fold-change | t |
|-------------------------------|--|------------|--|-----------|-------------|--------|
| | SEQ ID | GenBank ID | GenBank Name | | | |
| N40141_at | 743 | N40141 | JM27 protein | | 17.4 | -7.64 |
| rc_N23730_s_at | 724 | N23730 | v-fos FBJ murine osteosarcoma viral oncogene homolog | | 10.8 | -7.54 |
| rc_AA463726_s_at | 386 | AA463726 | JM27 protein | | 10.0 | -6.56 |
| rc_N23352_s_at | 723 | N23352 | proenkephalin | | 10.0 | -4.53 |
| rc_H64493_f_at | 590 | H64493 | immunoglobulin heavy constant gamma 3 (G3m marker) | | 9.1 | -4.36 |
| V01512_ma1_at | 993 | V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | | 9.1 | -7.40 |
| rc_H05704_r_at | 549 | H05704 | HCR (a-helix coiled-coil rod homologue) | | 8.1 | -2.79 |
| L49169_at | 649 | L49169 | FBJ murine osteosarcoma viral oncogene homolog B | | 8.0 | -5.81 |
| rc_AA410383_at | 277 | AA410383 | B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1) | | 7.5 | -3.95 |
| rc_AA131322_s_at | 74 | AA131322 | tryptase, alpha,tryptase, beta (tryptase II) | | 7.2 | -2.81 |
| R56183_s_at | 844 | R56183 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | | 6.9 | -2.77 |
| rc_AA461300_at | 381 | AA461300 | ESTs | | 6.9 | -7.08 |
| J00231_f_at | 617 | J00231 | immunoglobulin heavy constant gamma 3 (G3m marker) | | 6.7 | -4.62 |
| rc_AA427622_s_at | 311 | AA427622 | collagen, type XIII, alpha 1 | | 6.6 | -8.25 |
| rc_T90889_at | 927 | T90889 | ESTs | | 5.6 | -3.72 |
| rc_AA402903_f_at | 263 | AA402903 | immunoglobulin heavy constant gamma 3 (G3m marker) | | 5.6 | -3.61 |
| rc_T23622_at | 886 | T23622 | ESTs | | 5.5 | -5.24 |
| rc_T62857_at | 903 | T62857 | ESTs | | 5.4 | -7.85 |
| rc_AA256268_at | 175 | AA256268 | ESTs | | 5.3 | -6.86 |
| rc_R44714_s_at | 837 | R44714 | ESTs | | 5.3 | -4.83 |
| rc_AA236476_at | 154 | AA236476 | transmembrane protein TENB2, | | 5.1 | -3.13 |
| rc_AA028092_s_at | 17 | AA028092 | transcription factor 21 | | 5.1 | -5.24 |
| rc_T90619_f_at | 926 | T90619 | actin, gamma 1 | | 5.0 | -2.19 |
| J00123_at | 616 | J00123 | proenkephalin | | 5.0 | -3.96 |
| X52541_at | 1064 | X52541 | early growth response 1 | | 4.9 | -5.78 |
| rc_AA620825_at | 454 | AA620825 | CGI-43 protein | | 4.9 | -4.59 |
| rc_AA424530_s_at | 304 | AA424530 | ESTs | | 4.9 | -5.42 |
| rc_AA386386_s_at | 246 | AA386386 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) | | 4.9 | -2.64 |
| U62015_at | 978 | U62015 | cysteine-rich, angiogenic inducer, 61 | | 4.9 | -6.24 |
| rc_AA188981_at | 112 | AA188981 | highly expressed in cancer, rich in leucine heptad repeats | | 4.9 | -6.67 |
| rc_H21814_f_at | 563 | H21814 | immunoglobulin lambda locus | | 4.9 | -2.67 |
| M60314_at | 692 | M60314 | bone morphogenetic protein 5 | | 4.7 | -10.82 |
| rc_T67053_f_at | 909 | T67053 | immunoglobulin lambda locus | | 4.7 | -2.84 |
| rc_N47686_s_at | 744 | N47686 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | | 4.7 | -3.27 |
| rc_AA436616_at | 335 | AA436616 | ESTs | | 4.7 | -6.34 |
| rc_H60595_s_at | 585 | H60595 | progesterone binding protein | | 4.7 | -2.66 |
| rc_H88338_at | 601 | H88338 | ESTs | | 4.7 | -7.93 |
| M33653_at | 682 | M33653 | collagen, type XIII, alpha 1 | | 4.6 | -8.95 |
| rc_N30198_at | 733 | N30198 | ESTs | | 4.5 | -5.87 |
| D83018_at | 513 | D83018 | nel (chicken)-like 2 | | 4.5 | -9.79 |
| rc_Z39904_at | 1111 | Z39904 | ESTs | | 4.5 | -6.27 |
| H61295_s_at | 586 | H61295 | CD4 antigen (p55) | | 4.4 | -4.49 |
| rc_AA281345_f_at | 201 | AA281345 | immediate early protein | | 4.3 | -6.62 |
| rc_T23490_s_at | 885 | T23490 | hypothetical protein FLJ20185 | | 4.2 | -5.25 |
| rc_AA279760_at | 193 | AA279760 | DKFZP564M182 protein | | 4.2 | -3.73 |
| rc_R25410_at | 814 | R25410 | ESTs | | 4.2 | -4.69 |
| rc_T03229_f_at | 874 | T03229 | ESTs | | 4.2 | -3.37 |
| rc_R93908_at | 865 | R93908 | ESTs | | 4.2 | -3.39 |
| AA374109_at | 241 | AA374109 | spondin 2, extracellular matrix protein | | 4.2 | -1.97 |
| rc_R45654_at | 838 | R45654 | collagen, type XIII, alpha 1 | | 4.2 | -5.69 |
| rc_H86112_f_at | 600 | H86112 | KIAA0471 gene product | | 4.1 | -4.00 |
| rc_AA257093_r_at | 178 | AA257093 | T cell receptor beta locus | | 4.1 | -7.77 |
| rc_AA456147_at | 371 | AA456147 | general transcription factor IIIA | | 4.1 | -6.23 |

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|------------------|------|---------------|--|-----|-------|
| U21128_at | 953 | U21128 | lumican | 4.1 | -6.15 |
| rc_AA057195_at | 47 | AA057195 | TNF? elastin microfibril interface located protein | 4.1 | -2.22 |
| M63438_s_at | 696 | M63438 | immunoglobulin kappa variable 1D-8 | 4.0 | -2.53 |
| M57466_s_at | 690 | M57466 | major histocompatibility complex, class II, DP beta 1 | 4.0 | -3.91 |
| rc_AA443923_at | 344 | AA443923 | cat eye syndrome critical region gene 1 | 4.0 | -3.01 |
| rc_N39415_at | 742 | N39415 | DKFZP586P2421 protein | 4.0 | -5.70 |
| rc_W67225_at | 1021 | W67225 | KIAA0592 protein | 4.0 | -3.35 |
| M62831_at | 695 | M62831 | immediate early protein | 4.0 | -6.39 |
| rc_AA404957_at | 266 | AA404957 | matrix Gla protein | 4.0 | -3.84 |
| rc_F02992_at | 526 | F02992 | ESTs | 4.0 | -3.65 |
| U69263_at | 982 | U69263 | matrilin 2 | 3.9 | -4.84 |
| rc_AA448625_at | 354 | AA448625 | slit (Drosophila) homolog 3 | 3.9 | -4.13 |
| X57025_at | 1066 | X57025 | insulin-like growth factor 1 (somatomedin C) | 3.9 | -3.93 |
| AA151544_at | 91 | AA151544 | matrix metalloproteinase 23B | 3.8 | -5.54 |
| rc_F13763_at | 542 | F13763 | ESTs | 3.8 | -6.39 |
| rc_AA436655_at | 337 | AA436655 | hypothetical protein FLJ10781 | 3.8 | -5.13 |
| M87789_s_at | 704 | M87789 | immunoglobulin heavy constant gamma 3 (G3m marker) | 3.8 | -3.93 |
| L44416_at | 647 | L44416 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) | 3.8 | -1.75 |
| U20350_at | 951 | U20350 | chemokine (C-X3-C) receptor 1 | 3.8 | -6.50 |
| rc_AA449749_at | 355 | AA449749 | ESTs | 3.8 | -4.52 |
| rc_W73790_f_at | 1027 | W73790 | immunoglobulin lambda-like polypeptide 1 | 3.7 | -2.95 |
| rc_AA281145_at | 200 | AA281145 | ESTs | 3.7 | -1.77 |
| rc_f09748_s_at | 536 | F09748 | ESTs | 3.7 | -4.12 |
| rc_T64211_at | 906 | T64211 | HNOEL-iso protein | 3.7 | -5.35 |
| rc_N80152_at | 786 | N80152 | RNA binding motif protein 6 | 3.7 | -2.40 |
| rc_AA436618_at | 336 | AA436618 | microtubule-associated protein 2 | 3.7 | -4.67 |
| T85532_f_at | 917 | T85532 | ESTs | 3.7 | -1.90 |
| rc_AA398280_at | 248 | AA398280 | ESTs | 3.6 | -3.11 |
| rc_T23468_at | 884 | T23468 | CGI-119 protein | 3.6 | -4.67 |
| AA195678_at | 117 | AA195678 | actin binding protein; macrophin (microfilament and actin filament cross-linker protein) | 3.6 | -3.48 |
| AB002335_at | 460 | AB002335 | KIAA0337 gene product | 3.6 | -4.21 |
| rc_AA598982_s_at | 429 | AA598982 | KIAA1114 protein, trophinin | 3.6 | -4.58 |
| J03507_at | 621 | J03507 | complement component 7 | 3.6 | -6.21 |
| J04130_s_at | 625 | J04130 | small inducible cytokine A4 (homologous to mouse Mip-1b) | 3.5 | -4.76 |
| AA495865_at | 421 | AA495865 | ESTs | 3.5 | -3.65 |
| HG3543-HT3739_at | | HG3543-HT3739 | insulin-like growth factor 2 (somatomedin A) | 3.5 | -4.69 |
| rc_AA599662_s_at | 439 | AA599662 | KIAA0534 protein | 3.5 | -4.32 |
| rc_AA486072_i_at | 410 | AA486072 | small inducible cytokine A5 (RANTES) | 3.5 | -3.88 |
| rc_Z39983_s_at | 1112 | Z39983 | KIAA0561 protein | 3.5 | -5.56 |
| rc_F02333_at | 523 | F02333 | hypothetical protein FLJ20093 | 3.5 | -2.23 |
| rc_AA151210_at | 89 | AA151210 | ESTs | 3.5 | -4.20 |
| rc_N92239_at | 793 | N92239 | Wnt inhibitory factor-1 | 3.5 | -3.06 |
| rc_AA173223_at | 108 | AA173223 | ESTs | 3.5 | -5.22 |
| rc_T86148_s_at | 919 | T86148 | pituitary tumor-transforming 1 interacting protein | 3.5 | -2.15 |
| AA214688_at | 129 | AA214688 | eukaryotic translation initiation factor 4B | 3.5 | -3.13 |
| rc_AA216589_at | 131 | AA216589 | ESTs | 3.5 | -4.40 |
| rc_AA446661_at | 347 | AA446661 | hypothetical protein FLJ10970 | 3.4 | -3.69 |
| AA082546_at | 54 | AA082546 | ESTs | 3.4 | -4.12 |
| rc_W46395_at | 1009 | W46395 | chromobox homolog 6 | 3.4 | -2.41 |
| rc_AA401433_at | 257 | AA401433 | ESTs | 3.4 | -3.17 |
| D62965_at | 502 | D62965 | ESTs | 3.4 | -2.07 |
| rc_AA057829_s_at | 48 | AA057829 | growth arrest-specific 6 | 3.4 | -2.00 |
| rc_AA009755_at | 6 | AA009755 | ESTs | 3.3 | -4.77 |
| AA247204_at | 163 | AA247204 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 | 3.3 | -2.85 |
| D13628_at | 476 | D13628 | angiopoietin 1 | 3.3 | -4.86 |
| rc_N59866_at | 761 | N59866 | ESTs | 3.3 | -4.39 |
| rc_AA406371_at | 273 | AA406371 | ESTs | 3.3 | -4.98 |
| rc_N67876_s_at | 773 | N67876 | insulin-like growth factor 1 (somatomedin C) | 3.3 | -3.06 |

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|------------------|------|----------|--|-----|-------|
| M84526_at | 703 | M84526 | D component of complement (adipsin) | 3.3 | -3.06 |
| rc_AA234095_at | 144 | AA234095 | hypothetical protein FLJ20701 | 3.3 | -3.78 |
| rc_D60074_s_at | 498 | D60074 | cadherin 10 (T2-cadherin) | 3.3 | -5.05 |
| rc_T49602_s_at | 896 | T49602 | ESTs | 3.3 | -3.36 |
| rc_n22006_s_at | 718 | N22006 | ESTs | 3.3 | -3.88 |
| rc_F04112_f_at | 530 | F04112 | ESTs | 3.3 | -3.26 |
| rc_T64223_s_at | 907 | T64223 | carboxypeptidase A3 (mast cell) | 3.3 | -2.97 |
| U23946_at | 955 | U23946 | RNA binding motif protein 5 | 3.2 | -3.48 |
| rc_AA358038_at | 238 | AA358038 | SH3-binding domain glutamic acid-rich protein like | 3.2 | -3.21 |
| rc_AA019433_at | 12 | AA019433 | ESTs | 3.2 | -3.88 |
| X03689_s_at | 1044 | X03689 | eukaryotic translation elongation factor 1 alpha 1 | 3.2 | -1.91 |
| rc_H17550_at | 559 | H17550 | ESTs | 3.2 | -2.90 |
| rc_AA047880_at | 38 | AA047880 | prothymosin, alpha (gene sequence 28) | 3.2 | -5.88 |
| rc_AA084138_at | 55 | AA084138 | ESTs | 3.2 | -7.93 |
| rc_AA599365_at | 434 | AA599365 | decorin | 3.2 | -4.42 |
| rc_N91971_f_at | 791 | N91971 | retinol-binding protein 1, cellular | 3.2 | -4.13 |
| rc_T62873_at | 904 | T62873 | ESTs | 3.2 | -2.12 |
| rc_N49899_at | 746 | N49899 | ESTs | 3.2 | -3.73 |
| AA298981_at | 226 | AA298981 | fibulin 5 | 3.2 | -6.06 |
| rc_AA479286_at | 403 | AA479286 | ESTs | 3.2 | -3.54 |
| J04111_at | 624 | J04111 | v-jun avian sarcoma virus 17 oncogene homolog | 3.2 | -5.47 |
| rc_AA465491_at | 391 | AA465491 | Mad4 homolog | 3.2 | -2.75 |
| W28548_at | 997 | W28548 | ESTs | 3.2 | -3.59 |
| AA308998_at | 227 | AA308998 | endothelial differentiation-related factor 1 | 3.2 | -2.89 |
| rc_AA488432_at | 412 | AA488432 | phosphoserine phosphatase | 3.2 | -3.48 |
| rc_AA598991_at | 430 | AA598991 | amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) | 3.1 | -4.51 |
| AA463311_at | 384 | AA463311 | hypothetical protein similar to mouse Fbw5 | 3.1 | -2.57 |
| rc_AA147224_at | 85 | AA147224 | ESTs | 3.1 | -4.41 |
| rc_AA609504_at | 444 | AA609504 | fibronectin leucine rich transmembrane protein 2 | 3.1 | -3.81 |
| U20734_s_at | 952 | U20734 | jun B proto-oncogene | 3.1 | -3.37 |
| U06863_at | 941 | U06863 | follistatin-like 1 | 3.1 | -2.48 |
| W51743_at | 1011 | W51743 | ESTs | 3.1 | -2.95 |
| rc_AA465093_at | 389 | AA465093 | TIA1 cytotoxic granule-associated RNA-binding protein | 3.1 | -5.34 |
| rc_AA219100_at | 132 | AA219100 | DKFZP586P2421 protein | 3.1 | -4.09 |
| rc_R42424_at | 832 | R42424 | ESTs | 3.1 | -3.82 |
| rc_W73038_at | 1026 | W73038 | ESTs | 3.1 | -2.23 |
| AA091278_at | 60 | AA091278 | hypothetical protein FLJ10793 | 3.1 | -2.75 |
| rc_AA620289_at | 451 | AA620289 | PRO0518 protein | 3.1 | -2.55 |
| rc_AA149579_at | 87 | AA149579 | prostate cancer associated protein 1 | 3.1 | -2.66 |
| M21121_at | 668 | M21121 | small inducible cytokine A5 (RANTES) | 3.1 | -4.97 |
| rc_AA427890_at | 312 | AA427890 | ESTs | 3.1 | -4.32 |
| M34516_r_at | 684 | M34516 | immunoglobulin lambda-like polypeptide 1 | 3.1 | -3.47 |
| rc_AA233347_at | 140 | AA233347 | zinc finger protein 216 | 3.1 | -2.43 |
| rc_W74533_at | 1029 | W74533 | latrophilin | 3.1 | -3.51 |
| rc_AA029597_at | 19 | AA029597 | bone morphogenetic protein 7 (osteogenic protein 1) | 3.1 | -3.80 |
| rc_N91887_s_at | 790 | N91887 | thymosin, beta, identified in neuroblastoma cells | 3.1 | -4.47 |
| rc_AA205724_at | 123 | AA205724 | ESTs | 3.0 | -6.70 |
| U30521_at | 960 | U30521 | P311 protein | 3.0 | -6.06 |
| X07109_at | 1052 | X07109 | protein kinase C, beta 1 | 3.0 | -4.90 |
| D82346_at | 511 | D82346 | potassium voltage-gated channel, KQT-like subfamily, member 2 | 3.0 | -3.49 |
| rc_AA478962_at | 400 | AA478962 | ESTs | 3.0 | -3.35 |
| rc_AA151428_s_at | 90 | AA151428 | matrix metalloproteinase 23A,matrix metalloproteinase 23B | 3.0 | -2.78 |
| rc_AA130349_at | 73 | AA130349 | ESTs | 3.0 | -2.01 |
| M18737_ma1_at | 661 | M18737 | granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) | 3.0 | -5.90 |
| rc_N91461_at | 789 | N91461 | ESTs | 3.0 | -3.43 |
| rc_AA045481_at | 30 | AA045481 | ESTs | 3.0 | -3.70 |
| U91903_at | 989 | U91903 | frizzled-related protein | 3.0 | -4.73 |

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|------------------|------|----------|---|-----|-------|
| U19495_s_at | 950 | U19495 | stromal cell-derived factor 1 | 3.0 | -4.38 |
| M33493_s_at | 680 | M33493 | tryptase, alpha,tryptase, beta (tryptase II) | 3.0 | -3.12 |
| Y12711_at | 1103 | Y12711 | progesterone binding protein | 3.0 | -2.33 |
| rc_N58172_at | 757 | N58172 | ESTs | 3.0 | -2.53 |
| • M12529_at | 655 | M12529 | apolipoprotein E | 3.0 | -1.92 |
| rc_AA412505_at | 288 | AA412505 | ESTs | 3.0 | -3.35 |
| U45955_at | 967 | U45955 | glycoprotein M6B | 3.0 | -4.09 |
| rc_H56673_at | 581 | H56673 | ESTs | 3.0 | -4.25 |
| L33799_at | 645 | L33799 | procollagen C-endopeptidase enhancer | 3.0 | -4.72 |
| rc_Z40186_at | 1114 | Z40186 | ESTs | 3.0 | -2.22 |
| AA094800_at | 64 | AA094800 | eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) | 2.9 | -2.56 |
| D21063_at | 480 | D21063 | minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) | 2.9 | -5.27 |
| rc_AA412049_at | 284 | AA412049 | ESTs | 2.9 | -2.63 |
| rc_AA599661_at | 438 | AA599661 | ESTs | 2.9 | -8.62 |
| L02870_s_at | 633 | L02870 | collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive) | 2.9 | -4.69 |
| rc_AA232266_s_at | 138 | AA232266 | ESTs | 2.9 | -3.22 |
| L02321_at | 631 | L02321 | glutathione S-transferase M5 | 2.9 | -3.33 |
| rc_AA428325_at | 315 | AA428325 | SEC14 (S. cerevisiae)-like 2 | 2.9 | -3.52 |
| D82534_at | 512 | D82534 | f-box and leucine-rich repeat protein 5 | 2.9 | -2.20 |
| rc_T32113_at | 889 | T32113 | KIAA0657 protein | 2.9 | -2.47 |
| rc_R10896_at | 808 | R10896 | cytochrome c oxidase subunit VIIa polypeptide 2 like | 2.9 | -1.99 |
| rc_AA019034_i_at | 11 | AA019034 | ESTs | 2.9 | -4.40 |
| D28423_at | 485 | D28423 | ESTs | 2.9 | -2.31 |
| rc_AA609943_at | 449 | AA609943 | ESTs | 2.9 | -3.86 |
| W69302_at | 1023 | W69302 | ESTs | 2.9 | -2.68 |
| rc_H01824_f_at | 544 | H01824 | GATA-binding protein 2 | 2.9 | -3.82 |
| rc_T67105_s_at | 910 | T67105 | ESTs | 2.9 | -5.49 |
| rc_AA426372_s_at | 307 | AA426372 | H1 histone family, member X | 2.9 | -2.53 |
| rc_T98288_f_at | 933 | T98288 | ESTs | 2.9 | -2.66 |
| rc_N63047_at | 762 | N63047 | ESTs | 2.9 | -5.25 |
| U57316_at | 974 | U57316 | GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 | 2.9 | -3.59 |
| rc_AA219304_s_at | 133 | AA219304 | alpha-2-macroglobulin | 2.9 | -1.76 |

| TABLE 4 Affymetrix element | Normal vs. BPH W/Symptoms Table (Down-regulated) | | | 1678620.1 | t |
|-------------------------------|--|---------------|--|-------------|------|
| | SEQ ID | GenBank ID | GenBank Name | Fold-change | |
| rc_T40895_at | NO: 892 | T40895 | protein tyrosine phosphatase type IVA, member 1 | 16.5 | 5.19 |
| rc_N80129_i_at | 785 | N80129 | metallothionein 1L | 12.6 | 3.54 |
| rc_AA460914_at | 380 | AA460914 | ESTs | 7.4 | 4.58 |
| rc_AA234996_s_at | 147 | AA234996 | cytochrome c oxidase subunit VIa polypeptide 2 | 7.2 | 4.10 |
| X66141_at | 1078 | X66141 | myosin, light polypeptide 2, regulatory, cardiac, slow | 6.6 | 3.80 |
| AA234634_f_at | 145 | AA234634 | CCAAT/enhancer binding protein (C/EBP), delta | 6.2 | 4.35 |
| rc_AA419011_at | 296 | AA419011 | prostate androgen-regulated transcript 1 | 6.1 | 3.87 |
| rc_N94303_at | 797 | N94303 | ESTs | 5.8 | 5.96 |
| M20543_at | 666 | M20543 | actin, alpha 1, skeletal muscle | 5.5 | 3.20 |
| rc_AA085943_s_at | 58 | AA085943 | troponin T1, skeletal, slow | 5.5 | 3.02 |
| X06825_at | 1050 | X06825 | tropomyosin 2 (beta) | 5.2 | 3.35 |
| AB000584_at | 459 | AB000584 | prostate differentiation factor | 5.1 | 3.80 |
| M19309_s_at | 665 | M19309 | troponin T1, skeletal, slow | 5.0 | 3.41 |
| rc_AA040433_at | 24 | AA040433 | DKFZP586N2124 protein | 5.0 | 2.62 |
| rc_N32748_at | 736 | N32748 | ESTs | 5.0 | 3.36 |
| rc_AA227926_at | 135 | AA227926 | ESTs | 4.8 | 5.39 |
| rc_AA457566_at | 375 | AA457566 | ESTs | 4.7 | 4.22 |
| rc_AA026641_s_at | 16 | AA026641 | secretory leukocyte protease inhibitor (antileukoproteinase) | 4.6 | 2.09 |
| rc_AA053424_at | 40 | AA053424 | serine/threonine protein kinase MASK | 4.5 | 4.16 |
| V00594_at | 992 | V00594 | metallothionein 2A | 4.5 | 3.71 |
| rc_R16983_at | 811 | R16983 | ESTs | 4.5 | 3.23 |
| U75272_s_at | 984 | U75272 | progastricsin (pepsinogen C) | 4.4 | 4.57 |
| rc_T94447_s_at | 928 | T94447 | cortic al thymocyte receptor (X. laevis CTX) like | 4.4 | 3.50 |
| U08021_at | 942 | U08021 | nicotinamide N-methyltransferase | 4.4 | 2.41 |
| J03910_rna1_at | 622 | J03910 | metallothionein 1G | 4.3 | 2.79 |
| rc_AA236545_at | 156 | AA236545 | ESTs | 4.2 | 2.41 |
| rc_AA211443_at | 127 | AA211443 | ESTs | 4.2 | 4.49 |
| rc_AA398908_at | 251 | AA398908 | ESTs | 4.2 | 2.64 |
| X57129_at | 1067 | X57129 | H1 histone family, member 2 | 4.2 | 3.88 |
| M21665_s_at | 670 | M21665 | myosin, heavy polypeptide 7, cardiac muscle, beta | 4.1 | 3.61 |
| X65614_at | 1076 | X65614 | S100 calcium-binding protein P | 4.1 | 4.03 |
| rc_AA197112_r_at | 119 | AA197112 | putative nuclear protein | 4.1 | 3.07 |
| M99487_at | 716 | M99487 | folate hydrolase (prostate-specific membrane antigen) 1 | 4.0 | 2.65 |
| X04201_at | 1045 | X04201 | neurotrophic tyrosine kinase, receptor, type 1 | 3.9 | 2.87 |
| X05451_s_at | 1046 | X05451 | ESTs | 3.9 | 3.26 |
| rc_AA435720_i_at | 328 | AA435720 | tubulin, alpha 2 | 3.9 | 2.20 |
| rc_N92502_s_at | 794 | N92502 | ESTs | 3.8 | 3.11 |
| L77701_at | 651 | L77701 | COX17 (yeast) homolog, cytochrome c oxidase assembly protein | 3.8 | 3.97 |
| HG2157-HT2227_at | | HG2157-HT2227 | ESTs | 3.8 | 4.08 |
| X76717_at | 1087 | X76717 | metallothionein 1L | 3.8 | 5.82 |
| HG1067-HT1067_r_at | | HG1067-HT1067 | ESTs | 3.7 | 3.02 |
| rc_AA599331_at | 433 | AA599331 | CGI-119 protein, uncharacterized bone marrow protein BM039 | 3.6 | 4.90 |
| M20642_s_at | 667 | M20642 | ESTs | 3.6 | 3.48 |
| rc_AA055163_at | 44 | AA055163 | calsequestrin 2, cardiac muscle | 3.6 | 3.66 |
| rc_AA127946_at | 72 | AA127946 | DKFZP586B2022 protein | 3.6 | 4.40 |
| rc_AA022886_at | 14 | AA022886 | retinal degeneration B beta | 3.6 | 3.51 |
| rc_AA342337_at | 231 | AA342337 | ESTs | 3.5 | 2.57 |
| X02544_at | 1042 | X02544 | orosomucoid 1 | 3.5 | 1.92 |
| rc_T73433_s_at | 912 | T73433 | angiotensinogen | 3.5 | 3.10 |
| M21494_at | 669 | M21494 | creatine kinase, muscle | 3.4 | 2.46 |
| rc_AA488072_s_at | 411 | AA488072 | cardiac ankyrin repeat protein | 3.4 | 2.78 |

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|------------------|------|----------|---|-----|------|
| rc_AA293187_s_at | 223 | AA293187 | B-cell CLL/lymphoma 3 | 3.4 | 1.62 |
| rc_AA599522_r_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | 3.4 | 3.03 |
| rc_AA405488_at | 268 | AA405488 | ESTs | 3.4 | 2.57 |
| rc_AA461453_at | 382 | AA461453 | calcium binding protein Cab45 precursor, | 3.4 | 3.10 |
| rc_AA609006_at | 440 | AA609006 | ESTs | 3.4 | 2.30 |
| rc_N24761_at | 725 | N24761 | TU12B1-TY protein | 3.4 | 3.89 |
| rc_AA432162_at | 324 | AA432162 | DKFZP586B2022 protein | 3.4 | 2.78 |
| X06256_at | 1047 | X06256 | integrin, alpha 5 (fibronectin receptor, alpha polypeptide) | 3.4 | 4.51 |
| rc_AA045825_at | 33 | AA045825 | ESTs | 3.3 | 3.90 |
| rc_AA478778_at | 399 | AA478778 | ESTs | 3.3 | 4.37 |
| rc_N80129_f_at | 785 | N80129 | metallothionein 1L | 3.2 | 3.60 |
| rc_AA182030_at | 110 | AA182030 | pyruvate dehydrogenase kinase, isoenzyme 4 | 3.2 | 3.72 |
| rc_AA102489_at | 67 | AA102489 | hypothetical protein FLJ10337 | 3.2 | 2.20 |
| rc_R46074_at | 840 | R46074 | transforming, acidic coiled-coil containing protein 2 | 3.2 | 3.38 |
| rc_AA599522_f_at | 437 | AA599522 | squamous cell carcinoma antigen recognised by T cells | 3.2 | 2.36 |
| rc_AA165313_at | 104 | AA165313 | ESTs | 3.2 | 2.76 |
| rc_AA429636_at | 319 | AA429636 | hexokinase 2 | 3.2 | 3.12 |
| rc_R71792_s_at | 855 | R71792 | thrombospondin 1 | 3.1 | 2.31 |
| U05861_at | 940 | U05861 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase),aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) | 3.1 | 2.62 |
| rc_AA410311_at | 275 | AA410311 | ESTs | 3.1 | 3.52 |
| rc_AA505136_at | 426 | AA505136 | ESTs | 3.1 | 3.00 |
| rc_T68873_f_at | 911 | T68873 | metallothionein 1L | 3.0 | 3.18 |
| X00371_rna1_at | 1041 | X00371 | myoglobin | 3.0 | 2.18 |
| rc_AA099820_at | 65 | AA099820 | ESTs | 3.0 | 3.08 |
| rc_T90190_s_at | 925 | T90190 | H1 histone family, member 2 | 3.0 | 3.48 |
| rc_AA227936_f_at | 136 | AA227936 | parathymosin | 3.0 | 1.76 |
| X90568_at | 1092 | X90568 | titin | 3.0 | 2.83 |
| rc_AA004699_at | 1 | AA004699 | orphan G-protein coupled receptor | 3.0 | 2.23 |
| rc_F03969_at | 528 | F03969 | ESTs | 2.9 | 2.53 |
| X93036_at | 1093 | X93036 | FXYD domain-containing ion transport regulator 3 | 2.9 | 2.91 |
| rc_R91484_at | 863 | R91484 | ESTs | 2.9 | 6.43 |
| rc_AA025370_at | 15 | AA025370 | KIAA0872 protein | 2.9 | 2.87 |
| X51441_s_at | 1063 | X51441 | serum amyloid A1 | 2.9 | 1.78 |
| X64177_f_at | 1075 | X64177 | metallothionein 1H | 2.9 | 3.36 |
| rc_AA255480_at | 173 | AA255480 | ECSIT | 2.9 | 2.38 |
| rc_AA476944_at | 394 | AA476944 | ESTs | 2.8 | 4.26 |
| U78294_at | 985 | U78294 | arachidonate 15-lipoxygenase, second type | 2.8 | 1.82 |
| rc_AA045487_at | 31 | AA045487 | ESTs | 2.8 | 2.75 |
| rc_N74291_at | 779 | N74291 | ESTs | 2.8 | 1.88 |
| rc_N91973_at | 792 | N91973 | hypothetical protein,three prime repair exonuclease 1 | 2.8 | 1.97 |
| D81655_at | 510 | D81655 | ESTs | 2.8 | 1.89 |
| U53225_at | 971 | U53225 | sorting nexin 1 | 2.8 | 3.16 |
| rc_H77597_f_at | 594 | H77597 | metallothionein 1H | 2.8 | 2.98 |
| K02215_at | 628 | K02215 | angiotensinogen | 2.8 | 3.05 |
| rc_AA464728_s_at | 388 | AA464728 | ESTs | 2.7 | 3.80 |
| rc_W49708_at | 1010 | W49708 | ESTs | 2.7 | 3.52 |
| rc_AA453435_at | 364 | AA453435 | ESTs | 2.7 | 4.78 |
| rc_D11824_at | 474 | D11824 | ESTs | 2.7 | 3.70 |
| rc_T56281_f_at | 902 | T56281 | RNA helicase-related protein | 2.7 | 2.62 |
| rc_AA182882_at | 111 | AA182882 | titin-cap (telethonin) | 2.7 | 1.85 |
| rc_AA447522_at | 349 | AA447522 | ESTs | 2.7 | 3.27 |
| rc_N26904_at | 731 | N26904 | FK506 binding protein precursor | 2.7 | 3.21 |
| rc_AA131919_at | 75 | AA131919 | putative type II membrane protein | 2.7 | 4.15 |
| rc_R89840_at | 862 | R89840 | ESTs | 2.7 | 2.23 |

| | | | | | |
|------------------|------|----------|---|-----|------|
| rc_W31470_at | 998 | W31470 | thyroid hormone receptor-associated protein, 95-kD subunit | 2.7 | 2.85 |
| rc_W92207_at | 1036 | W92207 | ESTs | 2.7 | 4.07 |
| U96094_at | 990 | U96094 | sarcolipin | 2.7 | 2.23 |
| rc_W70131_at | 1024 | W70131 | ESTs | 2.7 | 3.64 |
| rc_AA435720_f_at | 328 | AA435720 | tubulin, alpha 2 | 2.7 | 1.98 |
| rc_AA284879_at | 212 | AA284879 | ESTs | 2.7 | 1.74 |
| rc_H22453_at | 564 | H22453 | ESTs | 2.7 | 4.20 |
| D14826_s_at | 478 | D14826 | cAMP responsive element modulator | 2.6 | 4.13 |
| rc_N93798_at | 796 | N93798 | protein tyrosine phosphatase type IVA, member 3 | 2.6 | 3.12 |
| U41804_at | 965 | U41804 | putative T1/ST2 receptor binding protein | 2.6 | 4.37 |
| rc_W20486_f_at | 995 | W20486 | chromosome 21 open reading frame 56 | 2.6 | 2.74 |
| rc_AA055768_at | 45 | AA055768 | CGI-119 protein | 2.6 | 2.13 |
| rc_AA447977_s_at | 352 | AA447977 | ESTs | 2.6 | 3.22 |
| AA380393_at | 243 | AA380393 | SEC7 homolog | 2.6 | 2.29 |
| rc_N29568_at | 732 | N29568 | thyroid hormone receptor-associated protein, 150 kDa subunit | 2.6 | 2.46 |
| rc_AA426374_f_at | 308 | AA426374 | tubulin, alpha 2 | 2.6 | 3.20 |
| rc_H94471_at | 604 | H94471 | occludin | 2.6 | 2.19 |
| rc_AA252219_at | 169 | AA252219 | ESTs | 2.6 | 3.83 |
| rc_AA402000_at | 259 | AA402000 | ESTs | 2.6 | 2.29 |
| rc_Z38744_at | 1108 | Z38744 | putative gene product | 2.6 | 4.18 |
| AA045870_at | 34 | AA045870 | ESTs | 2.6 | 2.26 |
| rc_R38678_at | 823 | R38678 | ESTs | 2.6 | 4.16 |
| R39467_f_at | 826 | R39467 | NEU1 protein | 2.6 | 2.79 |
| AA455001_s_at | 368 | AA455001 | CGI-43 protein | 2.6 | 5.34 |
| rc_AA292328_at | 221 | AA292328 | activating transcription factor 5 | 2.6 | 2.88 |
| X57348_s_at | 1068 | X57348 | stratifin | 2.6 | 2.48 |
| rc_T95005_s_at | 929 | T95005 | ESTs | 2.5 | 3.30 |
| AA410355_at | 276 | AA410355 | ribosomal protein S6 kinase, 70kD, polypeptide | 2.5 | 2.31 |
| AA036900_at | 21 | AA036900 | ESTs | 2.5 | 2.45 |
| rc_F02204_at | 521 | F02204 | BAI1-associated protein 2 | 2.5 | 2.26 |
| U26173_s_at | 958 | U26173 | nuclear factor, interleukin 3 regulated | 2.5 | 3.91 |
| rc_AA477767_at | 396 | AA477767 | ESTs | 2.5 | 3.17 |
| rc_AA504805_s_at | 424 | AA504805 | interferon stimulated gene (20kD) | 2.5 | 3.79 |
| rc_R33627_i_at | 818 | R33627 | ESTs | 2.5 | 1.99 |
| rc_T40995_f_at | 893 | T40995 | alcohol dehydrogenase 3 (class I), gamma polypeptide | 2.5 | 2.15 |
| rc_R00144_at | 801 | R00144 | ESTs | 2.5 | 2.69 |
| U02020_at | 936 | U02020 | pre-B-cell colony-enhancing factor | 2.5 | 4.20 |
| rc_AA287832_at | 217 | AA287832 | ESTs | 2.5 | 3.80 |
| AA429539_f_at | 318 | AA429539 | hypothetical protein | 2.5 | 2.35 |
| rc_H05084_at | 547 | H05084 | GDP-mannose pyrophosphorylase B | 2.5 | 2.23 |
| rc_AA405616_at | 271 | AA405616 | ESTs | 2.5 | 3.33 |
| AA455381_at | 370 | AA455381 | aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) | 2.4 | 2.60 |
| M13955_at | 658 | M13955 | keratin 7 | 2.4 | 2.22 |
| rc_AA180314_at | 109 | AA180314 | ESTs | 2.4 | 2.53 |
| M37984_rna1_at | 688 | M37984 | troponin C, slow | 2.4 | 2.10 |
| M61764_at | 694 | M61764 | tubulin, gamma 1 | 2.4 | 3.48 |
| rc_AA150920_at | 88 | AA150920 | KIAA0539 gene product | 2.4 | 4.11 |
| X65965_s_at | 1077 | X65965 | superoxide dismutase 2, mitochondrial | 2.4 | 2.37 |
| X93510_at | 1094 | X93510 | LIM domain protein | 2.4 | 2.39 |
| rc_N48056_s_at | 745 | N48056 | folate hydrolase (prostate-specific membrane antigen) 1 | 2.4 | 1.80 |
| rc_N26713_s_at | 729 | N26713 | ESTs | 2.4 | 3.87 |
| rc_AA282247_at | 204 | AA282247 | ESTs | 2.4 | 3.17 |
| rc_D80617_at | 508 | D80617 | KIAA0596 protein | 2.4 | 2.02 |
| rc_F02245_at | 522 | F02245 | monoamine oxidase A | 2.4 | 2.79 |
| rc_R58878_at | 847 | R58878 | ESTs | 2.4 | 2.80 |
| rc_W45531_at | 1007 | W45531 | ESTs | 2.4 | 4.17 |
| L25270_at | 644 | L25270 | SMC (mouse) homolog, X chromosome | 2.4 | 3.26 |
| rc_W88568_at | 1035 | W88568 | glycogenin 2 | 2.4 | 1.90 |

| | | | | | |
|--------------------|------|---------------|--|-----|------|
| rc_AA070752_s_at | 51 | AA070752 | insulin receptor substrate 1 | 2.4 | 2.87 |
| U24169_at | 956 | U24169 | JTV1 gene,hypothetical protein PRO0992 | 2.4 | 3.41 |
| rc_T15423_s_at | 878 | T15423 | 2',3'-cyclic nucleotide 3' phosphodiesterase | 2.4 | 1.71 |
| X78706_at | 1088 | X78706 | carnitine acetyltransferase | 2.4 | 3.51 |
| rc_T10695_i_at | 876 | T10695 | enigma (LIM domain protein) | 2.4 | 1.52 |
| rc_AA430388_at | 321 | AA430388 | HSPC160 protein | 2.4 | 5.04 |
| M68519_ma1_at | 699 | M68519 | surfactant, pulmonary-associated protein A1 | 2.4 | 3.89 |
| rc_AA421562_at | 300 | AA421562 | anterior gradient 2 (<i>Xenopus laevis</i>) homolog | 2.4 | 1.80 |
| rc_T97243_at | 931 | T97243 | prenyl protein protease RCE1 | 2.4 | 2.46 |
| rc_T15409_f_at | 877 | T15409 | ESTs | 2.3 | 3.76 |
| rc_T62918_at | 905 | T62918 | ESTs | 2.3 | 2.59 |
| rc_R15108_at | 810 | R15108 | ESTs | 2.3 | 2.74 |
| AA454908_s_at | 366 | AA454908 | KIAA0144 gene product | 2.3 | 2.77 |
| rc_N64683_at | 764 | N64683 | CGI-119 protein | 2.3 | 2.27 |
| rc_H99035_at | 612 | H99035 | ESTs | 2.3 | 4.34 |
| Y08374_ma1_at | 1100 | Y08374 | chitinase 3-like 1 (cartilage glycoprotein-39) | 2.3 | 2.94 |
| rc_AA236241_at | 150 | AA236241 | ESTs | 2.3 | 1.57 |
| U52969_at | 970 | U52969 | Purkinje cell protein 4 | 2.3 | 3.49 |
| rc_R11526_f_at | 809 | R11526 | parathymosin | 2.3 | 1.71 |
| rc_T15850_f_at | 880 | T15850 | ESTs | 2.3 | 2.42 |
| HG2259-HT2348_s_at | | HG2259-HT2348 | tubulin, alpha 1 (testis specific),tubulin, alpha, ubiquitous | 2.3 | 2.91 |
| rc_H15143_s_at | 554 | H15143 | ortholog of rat pippin | 2.3 | 1.45 |
| rc_AA101767_at | 66 | AA101767 | ESTs | 2.3 | 3.52 |
| rc_AA193197_at | 116 | AA193197 | sarcomeric muscle protein | 2.3 | 1.98 |
| U03688_at | 938 | U03688 | cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) | 2.3 | 2.97 |
| rc_R37774_at | 822 | R37774 | cytochrome P450 retinoid metabolizing protein | 2.3 | 4.11 |
| rc_H81413_f_at | 597 | H81413 | high-mobility group (nonhistone chromosomal) protein isoforms I and Y | 2.3 | 3.12 |
| X16354_at | 1060 | X16354 | carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) | 2.3 | 2.54 |
| rc_AA457235_at | 373 | AA457235 | ESTs | 2.3 | 2.25 |
| D13643_at | 477 | D13643 | KIAA0018 gene product | 2.3 | 1.78 |
| rc_N30856_at | 734 | N30856 | solute carrier family 19 (thiamine transporter), member 2 | 2.3 | 3.45 |
| M26311_s_at | 673 | M26311 | S100 calcium-binding protein A9 (calgranulin B) | 2.3 | 2.37 |
| rc_Z40556_at | 1116 | Z40556 | CGI-96 protein | 2.3 | 2.39 |
| rc_N79070_at | 783 | N79070 | ESTs | 2.3 | 1.43 |
| Z69881_at | 1122 | Z69881 | ATPase, Ca++ transporting, ubiquitous | 2.3 | 3.87 |
| rc_D60755_s_at | 500 | D60755 | ESTs | 2.3 | 2.30 |
| rc_N94424_at | 798 | N94424 | retinoic acid receptor responder (tazarotene induced) 1 | 2.2 | 1.09 |

Table 5

Up-regulated genes

Down-regulated genes

| Cluster | Fragment Name | Cluster | Fragment Name |
|---------|-----------------------------|---------|--|
| 1 | rc_AA256268_at | 1 | rc_AA227926_at |
| 1 | rc_AA188981_at | 1 | rc_AA398908_at |
| 1 | rc_AA173223_at | 1 | L77701_at |
| 1 | rc_AA216589_at | 1 | rc_AA599331_at |
| 1 | rc_AA234095_at | 1 | AA455001_s_at |
| 1 | rc_H17550_at | 3 | rc_AA022886_at |
| 1 | AA308998_at | 3 | rc_N24761_at |
| 1 | rc_AA488432_at | 3 | X06256_at |
| 1 | rc_AA427890_at | 4 | HG1067-HT1067_r_at |
| 1 | rc_N91887_s_at | 4 | rc_AA127946_at |
| 1 | rc_AA045481_at | 4 | rc_AA405488_at |
| 3 | rc_T23622_at | 5 | AA234634_f_at |
| 3 | rc_T23490_s_at | 5 | X65614_at |
| 3 | rc_AA620289_at | 5 | rc_T73433_s_at |
| 4 | rc_H05704_r_at | 5 | rc_R91484_at |
| 4 | rc_AA436616_at | 5 | rc_N93798_at |
| 4 | rc_AA456147_at | 6 | rc_N94303_at |
| 4 | rc_f09748_s_at, AA495865_at | 6 | AB000584_at |
| 4 | rc_AA598982_s_at | 6 | rc_AA410311_at |
| 4 | HG3543-HT3739_at | 6 | rc_F02245_at |
| 4 | rc_AA609504_at | 7 | rc_T40895_at |
| 5 | rc_AA028092_s_at | 7 | rc_N80129_i_at, X76717_at, rc_N80129_f_at, rc_T68873_f_at |
| 5 | U62015_at | 7 | rc_N32748_at |
| 5 | rc_F13763_at | 7 | V00594_at |
| 5 | rc_AA205724_at | 7 | J03910_rna1_at |
| 5 | U30521_at | 7 | X57129_at, rc_T90190_s_at |
| 6 | X52541_at | 7 | rc_AA182030_at |
| 6 | rc_AA281345_f_at, M62831_at | 7 | rc_AA505136_at |
| 7 | rc_n22006_s_at | 7 | X64177_f_at, rc_H77597_f_at |
| 7 | rc_R42424_at | 7 | rc_AA101767_at |

TABLE 6 BPH vs. Normal and Cancer

1689495.1

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID AA092215 | GenBank Name potassium channel modulatory factor | P- Values | | | | | |
|-----------------------------|---------------|------------------------|---|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| AA092215_at | 61 | AA092215 | potassium channel modulatory factor | 0.1086431 | 0.887604969 | 0.000105867 | 0.141381127 | 0.031099165 | 0.000775399 |
| AA122242_at | 70 | AA122242 | mannose-6-phosphate receptor (cation dependent) | 7.49E-05 | 0.560180168 | 0.87992066 | 0.006231736 | 0.000301953 | 0.664273011 |
| AA122302_at | 71 | AA122302 | | 0.430127474 | 0.003373118 | 0.068806262 | 0.000514723 | 0.328161735 | 1.48715E-05 |
| AA155958_at | 94 | AA155958 | S164 protein | 0.096247016 | 0.007959573 | 0.170003368 | 8.36688E-05 | 0.782399153 | 0.000223021 |
| AA236286_at | 151 | AA236286 | fetal Alzheimer antigen | 0.052450894 | 0.034104742 | 0.076032207 | 0.000282858 | 0.875443134 | 0.000444882 |
| AA248802_at | 165 | AA248802 | DKFZP564A122 protein | 0.000230259 | 0.38257085 | 0.842458286 | 0.026030878 | 0.000947368 | 0.500601376 |
| AA293544_at | 225 | AA293544 | D component of complement (adipsin) | 7.02821E-05 | 0.203858328 | 0.178154822 | 5.9415E-06 | 0.012632481 | 0.019226603 |
| AA376468_at | 242 | AA376468 | | 0.405364589 | 0.000353844 | 0.537460601 | 0.006147013 | 0.169320077 | 7.97148E-05 |
| AA410925_at | 278 | AA410925 | transducin-like enhancer of split 1, homolog of Drosophila E(sp1) | 0.870505598 | 1.09859E-05 | 0.106359333 | 4.33855E-05 | 0.168431987 | 0.003967521 |
| AA461618_s_at | 383 | AA461618 | | 0.001614433 | 0.497688178 | 0.000768417 | 0.001055794 | 6.29856E-10 | 0.031759146 |
| C15965_at | 468 | C15965 | | 0.000459149 | 0.350724893 | 0.919693498 | 0.000138025 | 0.000627643 | 0.416397432 |
| D10537_s_at | 472 | D10537 | myelin protein zero (Charcot-Marie-Tooth neuropathy 1B) | 4.11477E-05 | 0.923679005 | 4.72641E-05 | 0.000899706 | 0.975645863 | 0.00098994 |
| D25303_at | 482 | D25303 | integrin, alpha 9 | 0.00061935 | 0.196221991 | 0.000846365 | 0.108182462 | 0.935105808 | 0.124782864 |
| D26598_at | 483 | D26598 | proteasome (prosome, macropain) subunit, beta type, 3 | 0.000121781 | 0.02105211 | 8.45942E-05 | 0.326778603 | 0.933101073 | 0.291769938 |
| D31887_at | 489 | D31887 | KIAA0062 protein | 0.000123265 | 0.125782983 | 0.000676946 | 0.084742928 | 0.675822922 | 0.174766454 |
| D50532_at | 492 | D50532 | macrophage lectin 2 (calcium dependent) | 0.013806312 | 0.034992941 | 0.07897755 | 0.981647465 | 6.26998E-05 | 0.000487842 |
| D50550_at | 493 | D50550 | lethal giant larvae (Drosophila) homolog 1 | 3.10455E-05 | 0.029363545 | 4.06139E-05 | 0.169772872 | 0.953324091 | 0.186302331 |
| D64154_at | 503 | D64154 | cell membrane glycoprotein, 110000M(r) (surface antigen) | 1.68633E-05 | 0.000696104 | 5.00873E-05 | 0.747380424 | 0.814285971 | 0.90759386 |
| D84294_at | 514 | D84294 | tetratricopeptide repeat domain 3 | 8.04076E-06 | 0.163620727 | 0.000752223 | 0.017501269 | 0.299205599 | 0.142785528 |
| D86976_at | 515 | D86976 | minor histocompatibility antigen HA-1 | 3.35538E-06 | 0.219311742 | 4.36833E-07 | 0.007209475 | 0.701246025 | 0.002498824 |
| D87258_at | 516 | D87258 | protease, serine, 11 (IGF binding) | 9.00737E-05 | 0.762310231 | 0.004565624 | 0.000386998 | 0.305696637 | 0.008038934 |
| D87292_at | 517 | D87292 | thiosulfate sulfurtransferase (rhodanese) | 0.004418719 | 0.000188241 | 0.000878154 | 0.222741306 | 0.648642702 | 0.412420863 |
| D87465_at | 518 | D87465 | KIAA0275 gene product | 7.37644E-05 | 0.826724125 | 0.000140053 | 0.000450807 | 0.882548967 | 0.000727958 |
| H19969_at | 562 | H19969 | | 0.005160656 | 7.47697E-07 | 6.71287E-07 | 0.01521142 | 0.039287107 | 0.535558762 |
| H61361_s_at | 587 | H61361 | immunoglobulin superfamily containing leucine-rich repeat | 4.92249E-05 | 0.834280925 | 5.95931E-05 | 0.001490555 | 0.966053313 | 0.001694157 |
| J00277_at | 618 | J00277 | v-Ha-ras Harvey rat sarcoma viral oncogene homolog | 0.035655118 | 0.055426457 | 0.009927846 | 0.000332747 | 0.650555821 | 6.72893E-05 |
| J04076_at | 623 | J04076 | early growth response 2 (Krox-20 (Drosophila) homolog) | 0.034912914 | 0.473833846 | 2.46869E-11 | 0.285997211 | 1.48067E-05 | 1.13903E-06 |
| J04605_at | 627 | J04605 | peptidase D | 0.000200727 | 0.006030981 | 0.000362209 | 0.648903631 | 0.885410388 | 0.742239283 |
| K03204_f_at | 630 | K03204 | proline-rich protein BstNI subfamily 1 | 0.283795673 | 0.000798814 | 0.913648897 | 0.019814734 | 0.26284107 | 0.000926711 |
| L02326_f_at | 632 | L02326 | | 0.105345943 | 0.659037818 | 6.62426E-05 | 0.076492051 | 0.02455672 | 0.000181614 |
| L05500_at | 635 | L05500 | adenylate cyclase 1 (brain) | 0.016699778 | 0.257619651 | 3.79921E-05 | 0.002077455 | 0.101519111 | 6.32745E-06 |
| L06797_s_at | 636 | L06797 | chemokine (C-X-C motif), receptor 4 (fusin) | 0.443118956 | 0.447152817 | 1.30523E-06 | 0.926525008 | 0.000111977 | 0.000981046 |
| L08246_at | 637 | L08246 | myeloid cell leukemia sequence 1 (BCL2- related) | 0.043208838 | 0.230033308 | 4.68128E-10 | 0.596833839 | 6.55684E-05 | 5.57731E-05 |
| L13740_at | 639 | L13740 | nuclear receptor subfamily 4, group A, member 1 | 0.791312753 | 0.872331125 | 8.60985E-05 | 0.70798804 | 7.00025E-05 | 0.001852799 |
| L13852_at | 640 | L13852 | ubiquitin-activating enzyme E1-like | 0.000578096 | 0.646204921 | 0.003882395 | 0.000950816 | 0.599103668 | 0.004460291 |
| L19437_at | 641 | L19437 | transaldolase 1 | 0.008021968 | 0.22883538 | 0.001388037 | 0.000773689 | 0.604482478 | 0.000135454 |

TABLE 6 BPH vs. Normal and Cancer

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID L34587 | GenBank Name transcription elongation factor B (SII), polypeptide 1 (15kD, elongin C) cyclic AMP phosphoprotein, 19 kD | P- Values | | | | | |
|-----------------------------|---------------|----------------------|--|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| L34587_at | 646 | L34587 | transcription elongation factor B (SII), polypeptide 1 (15kD, elongin C) | 0.000178315 | 0.105125832 | 7.09176E-05 | 0.11839964 | 0.830767426 | 0.080296411 |
| L44497_at | 648 | L44497 | cyclic AMP phosphoprotein, 19 kD | 0.000816364 | 0.012044336 | 0.000161685 | 0.709380948 | 0.686659704 | 0.467540879 |
| L76200_at | 650 | L76200 | guanylate kinase 1 | 0.000841699 | 0.002396122 | 0.000888336 | 0.889388751 | 0.988638065 | 0.879528075 |
| M12959_s_at | 656 | M12959 | T cell receptor alpha locus | 3.02601E-08 | 0.817611534 | 3.24058E-08 | 1.14437E-05 | 0.990909384 | 1.1981E-05 |
| M13560_s_at | 657 | M13560 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen- associated) | 0.01541788 | 0.255419127 | 4.82527E-06 | 0.001882075 | 0.041399052 | 9.73079E-07 |
| M14660_at | 659 | M14660 | | 1.95092E-06 | 0.823404837 | 0.009910008 | 0.000180501 | 0.038673415 | 0.053432817 |
| M16336_s_at | 660 | M16336 | CD2 antigen (p50), sheep red blood cell receptor | 0.000908965 | 0.444045616 | 0.000106508 | 0.042888317 | 0.596564762 | 0.01280799 |
| M19154_at | 663 | M19154 | transforming growth factor, beta 2 | 0.021033675 | 0.886661499 | 5.38416E-05 | 0.039706043 | 0.100571645 | 0.00047052 |
| M19283_at | 664 | M19283 | actin, gamma 1 | 0.009680549 | 0.975542421 | 1.35524E-05 | 0.029109597 | 0.094241798 | 0.000262549 |
| M21121_s_at | 668 | M21121 | small inducible cytokine A5 (RANTES) | 0.00011935 | 0.82444906 | 0.028900951 | 0.000639223 | 0.114726075 | 0.042253328 |
| M31776_s_at | 677 | M31776 | natriuretic peptide precursor B | 9.53305E-05 | 0.786764461 | 0.00132485 | 0.000453681 | 0.511730949 | 0.003376181 |
| M33552_at | 681 | M33552 | lymphocyte-specific protein 1 | 0.098325681 | 0.187562681 | 0.000373789 | 0.008253387 | 0.070738695 | 2.37353E-05 |
| M37766_at | 687 | M37766 | CD48 antigen (B-cell membrane protein) | 0.006750544 | 0.671986725 | 0.000173892 | 0.007796504 | 0.321364096 | 0.000414775 |
| M54927_at | 689 | M54927 | proteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated) | 0.0008203 | 0.071504547 | 0.000610665 | 0.292633338 | 0.938762949 | 0.26282367 |
| M59465_at | 691 | M59465 | tumor necrosis factor, alpha-induced protein 3 | 0.905275899 | 0.300604716 | 2.40334E-05 | 0.370512119 | 3.79139E-05 | 6.51796E-06 |
| M60459_at | 693 | M60459 | erythropoietin receptor | 5.33228E-07 | 0.001997812 | 2.00307E-06 | 0.229150396 | 0.804556624 | 0.324369463 |
| M73077_at | 701 | M73077 | glucocorticoid receptor DNA binding factor 1 | 4.33165E-05 | 0.026210722 | 7.3229E-05 | 0.205361352 | 0.906734945 | 0.244557908 |
| M89796_ma1_at | 705 | M89796 | membrane-spanning 4- domains, subfamily A, member 1 | 3.38097E-07 | 0.68414038 | 0.000659504 | 0.000116527 | 0.107834095 | 0.014565483 |
| M94077_at | 709 | M94077 | loricrin | 7.86788E-05 | 0.167396165 | 8.55841E-06 | 0.050135902 | 0.633682729 | 0.017465235 |
| M94547_at | 710 | M94547 | myosin light chain 2a | 0.000922884 | 0.001567598 | 0.000142192 | 0.778547965 | 0.641162082 | 0.898495047 |
| M95678_at | 712 | M95678 | phospholipase C, beta 2 | 2.65752E-06 | 0.741444839 | 0.00021566 | 0.000330645 | 0.344847831 | 0.005753116 |
| M96995_s_at | 713 | M96995 | growth factor receptor- bound protein 2 | 0.000451432 | 0.370687613 | 0.000417356 | 0.039514013 | 0.984237779 | 0.037882757 |
| M98447_ma1_at | 714 | M98447 | transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine- gamma- glutamyltransferase) | 0.101078475 | 0.000501168 | 0.49866517 | 0.047778543 | 0.027993512 | 9.36193E-05 |
| N24990_s_at | 728 | N24990 | | 0.000594989 | 0.692375474 | 0.833157714 | 0.001206749 | 0.00054518 | 0.837698657 |
| R08720_at | 805 | R08720 | hypothetical protein FLJ22609 | 0.384088189 | 0.004709624 | 0.405658837 | 0.000582614 | 0.970613897 | 0.000656156 |
| R33301_at | 817 | R33301 | | 0.263328276 | 0.008898636 | 0.324726425 | 0.000573184 | 0.899017203 | 0.000860093 |
| R39394_at | 825 | R39394 | E1B-55kDa-associated protein 5 | 0.000120098 | 0.165965093 | 0.159597216 | 5.8721E-06 | 0.020650662 | 0.012378795 |
| rc_AA004901_at | 2 | AA004901 | | 0.00013 | 0.114226367 | 0.898931127 | 2.58485E-06 | 0.000448774 | 0.104547963 |
| rc_AA005382_s_at | 3 | AA005382 | granzyme K (serine protease, granzyme 3; tryptase II) | 4.06793E-05 | 0.956799991 | 0.000100487 | 0.000772831 | 0.838991074 | 0.001451838 |
| rc_AA009615_at | 5 | AA009615 | | 7.69548E-05 | 0.013016412 | 0.000583037 | 0.368115762 | 0.625611179 | 0.634185041 |
| rc_AA010358_at | 7 | AA010358 | | 1.36211E-06 | 0.550401822 | 0.139035486 | 0.000570081 | 0.001477269 | 0.511053692 |
| rc_AA017547_r_at | 9 | AA017547 | hypothetical protein FLJ12387 similar to kinesin light chain | 0.989540408 | 0.214430361 | 0.000274727 | 0.228713943 | 0.000584071 | 2.44522E-05 |
| rc_AA018414_at | 10 | AA018414 | | 0.556560157 | 0.000998026 | 0.519992597 | 0.000281037 | 0.958086097 | 0.000217926 |
| rc_AA022615_at | 13 | AA022615 | RNA binding motif protein 9 | 0.000158793 | 0.509341291 | 0.263342589 | 0.000159018 | 0.011670476 | 0.117665916 |
| rc_AA037828_at | 22 | AA037828 | | 0.000583981 | 0.645542969 | 0.84290982 | 0.000955558 | 0.002108779 | 0.543978545 |
| rc_AA043196_at | 26 | AA043196 | SMC (mouse) homolog, X chromosome | 0.008527895 | 0.000983583 | 0.000257323 | 0.328438436 | 0.331116816 | 0.90061816 |

TABLE 6 BPH vs. Normal and Cancer

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID AA053267 | GenBank Name KIAA1023 protein | P- Values | | | | | |
|-----------------------------|---------------|------------------------|--|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| rc_AA053267_at | 39 | AA053267 | KIAA1023 protein | 0.000119181 | 0.288536772 | 0.388296579 | 2.42934E-05 | 0.004627114 | 0.082295734 |
| rc_AA053883_at | 41 | AA053883 | | 4.95718E-05 | 0.962839667 | 0.16054889 | 0.000624096 | 0.01179586 | 0.225390364 |
| rc_AA054222_at | 42 | AA054222 | | 0.39176403 | 0.002571399 | 0.102566251 | 0.000307234 | 0.461555799 | 2.09152E-05 |
| rc_AA055081_at | 43 | AA055081 | | 6.36828E-05 | 0.206434411 | 0.797911434 | 5.59851E-06 | 5.42681E-05 | 0.316914958 |
| rc_AA065173_at | 49 | AA065173 | chromosome 5 open reading frame 4 | 2.52678E-07 | 0.570857861 | 0.058275966 | 0.000180212 | 0.001970189 | 0.302526217 |
| rc_AA069913_at | 50 | AA069913 | | 0.653765843 | 0.52776555 | 5.65709E-06 | 0.815416554 | 0.000104293 | 0.00152505 |
| rc_AA071558_at | 52 | AA071558 | | 0.168309619 | 0.418677904 | 0.000189452 | 0.054446269 | 0.025471654 | 0.000103274 |
| rc_AA082041_at | 53 | AA082041 | likely homolog of rat kinase D-interacting substance of 220 kDa; KIAA1250 protein | 0.000143369 | 0.247732655 | 0.871515758 | 0.040056839 | 0.000552895 | 0.3290855 |
| rc_AA084324_at | 56 | AA084324 | | 0.000226203 | 0.056433291 | 0.000687497 | 0.216607531 | 0.780835192 | 0.321404997 |
| rc_AA085608_at | 57 | AA085608 | KIAA1041 protein | 0.029391584 | 0.03435634 | 0.041546789 | 0.000120442 | 0.894217078 | 0.000192545 |
| rc_AA114858_at | 68 | AA114858 | tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide | 0.000210292 | 0.155417252 | 0.994165585 | 8.63652E-06 | 0.000449478 | 0.170373425 |
| rc_AA132239_at | 76 | AA132239 | | 0.012168107 | 5.56988E-05 | 4.55236E-05 | 0.074087524 | 0.136307788 | 0.631558319 |
| rc_AA132453_at | 77 | AA132453 | | 0.000489304 | 0.141814616 | 8.74406E-05 | 0.136343527 | 0.678807616 | 0.063921338 |
| rc_AA136864_at | 81 | AA136864 | zinc finger protein homologous to Zfp-36 in mouse | 0.000224205 | 0.630168118 | 4.9041E-05 | 0.009114985 | 0.72551107 | 0.003549498 |
| rc_AA143190_s_at | 83 | AA143190 | CGI-147 protein | 5.31694E-05 | 0.028242427 | 0.000127165 | 0.209594394 | 0.842566905 | 0.279924929 |
| rc_AA143467_at | 84 | AA143467 | hypothetical protein FLJ20343 | 1.62361E-06 | 0.259338862 | 1.37865E-06 | 0.003657312 | 0.975267724 | 0.003351742 |
| rc_AA149051_at | 86 | AA149051 | | 4.08493E-05 | 0.490333235 | 0.026825837 | 4.57567E-05 | 0.07318676 | 0.012248149 |
| rc_AA152408_at | 93 | AA152408 | KIAA0433 protein | 2.97974E-05 | 0.362537361 | 0.455914763 | 1.36986E-05 | 0.001140199 | 0.13486533 |
| rc_AA156064_at | 95 | AA156064 | | 0.275270351 | 0.000333624 | 0.875633108 | 0.011111677 | 0.23661308 | 0.000347347 |
| rc_AA158132_at | 98 | AA158132 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 | 0.004899515 | 0.643469716 | 4.65182E-07 | 0.057915819 | 0.034659352 | 0.000177571 |
| rc_AA165116_at | 101 | AA165116 | | 0.000384885 | 0.681603266 | 0.211571862 | 0.000813512 | 0.029042963 | 0.151679697 |
| rc_AA165231_at | 102 | AA165231 | | 0.002549485 | 0.173959444 | 0.254670513 | 0.000135147 | 8.0406E-05 | 0.719982481 |
| rc_AA169837_at | 105 | AA169837 | NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH- coenzyme Q reductase) | 0.08971279 | 0.008766485 | 0.091371238 | 8.4903E-05 | 0.993409911 | 8.74977E-05 |
| rc_AA172188_at | 107 | AA172188 | protocadherin alpha 5 | 0.000667976 | 0.267150381 | 4.96881E-06 | 0.077589163 | 0.269599078 | 0.006273958 |
| rc_AA189015_at | 113 | AA189015 | aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia) | 0.083660421 | 0.006384313 | 1.64695E-08 | 0.237580015 | 0.000203416 | 0.037803249 |
| rc_AA192553_at | 115 | AA192553 | uncoupling protein 3 (mitochondrial, proton carrier) | 0.10098208 | 0.00017981 | 0.933630822 | 0.02546947 | 0.102059527 | 0.000244309 |
| rc_AA196549_at | 118 | AA196549 | | 0.001049524 | 0.569766558 | 0.000482225 | 0.001065463 | 0.839463674 | 0.000559925 |
| rc_AA205072_at | 120 | AA205072 | KIAA0980 protein | 0.000335755 | 0.586934845 | 0.684865398 | 0.000455367 | 0.002552925 | 0.389985886 |
| rc_AA205460_at | 122 | AA205460 | | 0.000108573 | 0.165439416 | 0.84259483 | 5.28568E-06 | 0.000494762 | 0.134180366 |
| rc_AA205947_at | 124 | AA205947 | HHGP protein | 0.000271962 | 0.552878143 | 0.70583219 | 0.000318994 | 0.001963327 | 0.376568675 |
| rc_AA207103_at | 125 | AA207103 | amiloride-sensitive cation channel 2, neuronal | 2.05331E-05 | 0.045239142 | 0.642629872 | 0.10526525 | 0.000317921 | 0.124103707 |
| rc_AA211300_at | 126 | AA211300 | KIAA0627 protein; Drosophila "multiple asters" (Mast)-like homolog 2 | 0.004445798 | 0.287777463 | 0.006200387 | 0.000703498 | 0.918638362 | 0.000971608 |
| rc_AA211835_s_at | 128 | AA211835 | MHC class II transactivator | 0.001672055 | 0.122505424 | 0.000371358 | 4.15083E-05 | 0.692673582 | 8.76636E-06 |
| rc_AA215379_at | 130 | AA215379 | | 7.98828E-05 | 0.366787682 | 0.194666913 | 3.33447E-05 | 0.012005727 | 0.051632715 |
| rc_AA228020_at | 137 | AA228020 | splicing factor (CC1.3) | 0.00047128 | 0.328754864 | 0.940819016 | 0.000119264 | 0.001167483 | 0.317270472 |
| rc_AA233545_at | 141 | AA233545 | AD-003 protein | 0.004492717 | 0.655215048 | 2.53288E-07 | 0.052976799 | 0.028149978 | 0.000113193 |
| rc_AA233854_at | 142 | AA233854 | S-phase kinase- associated protein 2 (p45) | 3.79954E-05 | 0.744241299 | 0.538817385 | 0.001845337 | 0.000884538 | 0.84309443 |
| rc_AA233935_at | 143 | AA233935 | | 0.000608235 | 0.578078963 | 0.30216801 | 0.00070772 | 0.023016587 | 0.163656536 |
| rc_AA234831_at | 146 | AA234831 | KIAA0788 protein | 0.000575081 | 0.410892837 | 0.954176902 | 0.000257285 | 0.000897188 | 0.457935122 |
| rc_AA236453_at | 152 | AA236453 | | 0.036687413 | 0.061484767 | 0.023140149 | 0.000407818 | 0.863002571 | 0.000227528 |
| rc_AA236477_at | 155 | AA236477 | KIAA1559 protein | 0.000207423 | 0.453577644 | 0.288868663 | 0.000140775 | 0.011962605 | 0.1090363 |
| rc_AA236822_at | 157 | AA236822 | KIAA1097 protein | 0.008052957 | 0.439727961 | 0.000891185 | 0.003207259 | 0.52319673 | 0.000453056 |

TABLE 6 BPH vs. Normal and Cancer

1669495.1

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | |
|-----------------------------|---------------|------------|--|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| rc_AA237011_at | 158 | AA237011 | ATP-binding cassette, sub-family F (GCN20), member 1 | 0.000202964 | 0.000263744 | 1.87304E-06 | 0.678815593 | 0.318565402 | 0.645008985 |
| rc_AA237034_at | 159 | AA237034 | golgi SNAP receptor complex member 2 | 2.31824E-05 | 0.319635059 | 3.30639E-08 | 0.010320292 | 0.220104139 | 0.000272212 |
| rc_AA243416_s_at | 160 | AA243416 | hypothetical protein, expressed in osteoblast | 0.033376619 | 4.72108E-05 | 0.469143753 | 0.032420785 | 0.182985166 | 0.000942701 |
| rc_AA243698_at | 161 | AA243698 | potassium channel modulatory factor | 0.06151528 | 0.302492952 | 0.000486853 | 0.010884151 | 0.124764794 | 9.91149E-05 |
| rc_AA243763_at | 162 | AA243763 | | 0.050706904 | 0.01206437 | 0.11555761 | 5.40095E-05 | 0.71829242 | 0.000198301 |
| rc_AA253361_at | 172 | AA253361 | | 0.000564229 | 0.000110501 | 0.010769519 | 0.397832434 | 0.394174789 | 0.11120186 |
| rc_AA255966_at | 174 | AA255966 | | 0.000512371 | 0.381782918 | 0.000368364 | 0.040324542 | 0.933794518 | 0.03373143 |
| rc_AA256486_at | 177 | AA256486 | CG1-141 protein | 0.053041853 | 0.519681482 | 0.000805238 | 0.025864118 | 0.179038095 | 0.000657368 |
| rc_AA258585_at | 180 | AA258585 | cadherin 19, type 2 | 8.77783E-08 | 0.008879695 | 3.84529E-06 | 0.0526509 | 0.488129443 | 0.183610483 |
| rc_AA258595_f_at | 181 | AA258595 | major histocompatibility complex, class II, DQ beta 1 | 0.056902737 | 0.411462581 | 1.12504E-05 | 0.017626477 | 0.018278908 | 8.86477E-06 |
| rc_AA262107_at | 183 | AA262107 | | 0.051109951 | 0.028221779 | 0.046925687 | 0.000190669 | 0.972441626 | 0.000168986 |
| rc_AA262349_at | 184 | AA262349 | hypothetical protein FLJ10628 | 0.023368538 | 0.075191389 | 0.000520191 | 0.000323092 | 0.25384504 | 4.28987E-06 |
| rc_AA262477_at | 185 | AA262477 | ribonuclease HI, large subunit | 0.843423091 | 0.000293418 | 0.145801246 | 0.000917609 | 0.233064808 | 0.023283635 |
| rc_AA262969_f_at | 186 | AA262969 | px19-like protein | 0.000697965 | 0.002321008 | 4.86461E-08 | 0.916139727 | 0.050019001 | 0.106622452 |
| rc_AA278757_at | 187 | AA278757 | KIAA1205 protein | 0.000807747 | 0.701913497 | 0.00019298 | 0.001603897 | 0.719959281 | 0.000521168 |
| rc_AA278887_at | 189 | AA278887 | | 4.77289E-05 | 0.000505268 | 0.002921534 | 0.966491221 | 0.300838621 | 0.386804461 |
| rc_AA279028_at | 190 | AA279028 | | 0.269683575 | 0.000110029 | 0.896242284 | 0.00515459 | 0.355782598 | 0.000309622 |
| rc_AA279774_at | 194 | AA279774 | | 0.028330552 | 0.004250917 | 0.09766388 | 4.84994E-06 | 0.610845854 | 3.70943E-05 |
| rc_AA279821_s_at | 195 | AA279821 | | 0.01541818 | 0.057056528 | 0.036000999 | 0.00012115 | 0.75748484 | 0.000352962 |
| rc_AA280297_at | 196 | AA280297 | | 0.004904401 | 0.069649547 | 0.030554618 | 4.43102E-05 | 0.537205763 | 0.000396218 |
| rc_AA280309_at | 197 | AA280309 | | 0.027919295 | 0.048777883 | 0.042451847 | 0.000197325 | 0.872357649 | 0.000341621 |
| rc_AA280617_at | 198 | AA280617 | | 0.020747951 | 0.100016813 | 0.006218315 | 0.000457645 | 0.687853962 | 0.000114895 |
| rc_AA282739_at | 205 | AA282739 | Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like) | 0.006885251 | 0.224885918 | 0.001928329 | 0.000638964 | 0.705244944 | 0.000179491 |
| rc_AA283091_at | 206 | AA283091 | KIAA1219 protein | 0.000391955 | 0.950383286 | 0.000147487 | 0.003849943 | 0.812656175 | 0.001947884 |
| rc_AA283772_at | 207 | AA283772 | replication factor C (activator 1) 5 (36.5kD) | 0.472125644 | 0.004274231 | 0.126899001 | 0.00082772 | 0.443684418 | 5.94032E-05 |
| rc_AA283774_at | 208 | AA283774 | | 0.634799287 | 0.001085136 | 0.774459677 | 0.000408559 | 0.858121118 | 0.000730937 |
| rc_AA283907_at | 209 | AA283907 | DC12 protein | 0.702306606 | 0.426110345 | 0.000364953 | 0.278959611 | 0.000181185 | 0.027738884 |
| rc_AA284777_at | 211 | AA284777 | | 0.00028958 | 0.613024306 | 0.843581256 | 0.0004624 | 0.001148934 | 0.515630593 |
| rc_AA286862_at | 214 | AA286862 | WD repeat domain 6 | 0.006465478 | 0.770956466 | 3.90332E-06 | 0.047019059 | 0.072475744 | 0.000368843 |
| rc_AA287107_s_at | 215 | AA287107 | zinc finger protein ZNF140-like protein | 0.000557513 | 0.647966939 | 0.168481176 | 0.000931348 | 0.049075778 | 0.113081619 |
| rc_AA287870_s_at | 218 | AA287870 | lymphotoxin beta (TNF superfamily, member 3) | 0.042868875 | 0.904123896 | 4.72641E-06 | 0.071763173 | 0.015492602 | 8.72095E-05 |
| rc_AA291970_at | 220 | AA291970 | lectomedin-2 | 0.133517759 | 0.00116479 | 0.062658963 | 1.25187E-05 | 0.731829127 | 3.02794E-06 |
| rc_AA292533_at | 222 | AA292533 | putative Rab5-interacting protein | 8.63268E-05 | 0.143959708 | 1.94797E-06 | 0.062483153 | 0.429586131 | 0.010599279 |
| rc_AA342918_at | 232 | AA342918 | hypothetical protein FLJ22313 | 0.000298568 | 0.534260232 | 0.802167146 | 0.015864864 | 0.000243847 | 0.42047475 |
| rc_AA347578_s_at | 234 | AA347578 | tubulin, beta polypeptide | 0.056066605 | 0.067322154 | 0.053415125 | 0.000815763 | 0.984081099 | 0.000765743 |
| rc_AA348446_at | 235 | AA348446 | | 0.00081514 | 0.498461887 | 0.002492252 | 0.000590962 | 0.75904915 | 0.001541743 |
| rc_AA349417_at | 236 | AA349417 | | 0.333508877 | 4.09468E-05 | 0.860387174 | 0.001709823 | 0.452900772 | 0.000147762 |
| rc_AA370867_at | 239 | AA370867 | | 0.000438073 | 0.000509149 | 0.076534621 | 0.678852203 | 0.097859647 | 0.062063558 |
| rc_AA371520_at | 240 | AA371520 | | 0.000956188 | 0.182406672 | 0.0004497 | 0.142299266 | 0.84509761 | 0.101288353 |
| rc_AA398719_at | 249 | AA398719 | homolog of rat nadrin | 0.005171893 | 0.312848506 | 0.003453438 | 0.000980065 | 0.903295813 | 0.000667115 |
| rc_AA399101_at | 252 | AA399101 | | 0.020406213 | 0.066006562 | 0.014033951 | 0.000219359 | 0.896140692 | 0.00013891 |
| rc_AA399542_f_at | 254 | AA399542 | | 0.225479535 | 0.502403493 | 5.62157E-05 | 0.098347881 | 0.007549959 | 6.44137E-05 |
| rc_AA400034_at | 255 | AA400034 | | 0.250995551 | 0.01453561 | 0.033099094 | 0.00095651 | 0.35107658 | 3.77436E-05 |
| rc_AA401297_s_at | 256 | AA401297 | symplekin; Huntingtin interacting protein I | 0.012585329 | 0.166831042 | 0.004370096 | 0.000663018 | 0.73639502 | 0.000215874 |
| rc_AA402468_at | 261 | AA402468 | | 0.099732216 | 9.36987E-05 | 0.673315411 | 0.017152495 | 0.245352826 | 0.000668187 |
| rc_AA402473_at | 262 | AA402473 | | 0.457960224 | 0.000426525 | 0.079152517 | 6.26915E-05 | 0.336346183 | 1.26194E-06 |
| rc_AA405331_at | 267 | AA405331 | golgi autoantigen, golgin subfamily a, 5 | 0.586184325 | 0.001885183 | 0.429082537 | 0.000584353 | 0.815182938 | 0.00026866 |
| rc_AA405533_at | 269 | AA405533 | integral membrane protein 2B | 0.000172614 | 0.497994468 | 0.082141472 | 0.000159183 | 0.055604922 | 0.0359498 |
| rc_AA405902_at | 272 | AA405902 | | 0.086820061 | 0.039035914 | 0.014052865 | 0.000655228 | 0.480598833 | 5.66656E-05 |
| rc_AA410954_at | 279 | AA41 | | | | | | | |

TABLE 6 BPH vs. Normal and Cancer

1669435.1

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | | |
|-----------------------------|---------------|------------|---|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|-------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer | |
| rc_AA412267_at | 286 | AA412267 | | 0.164103629 | 3.89169E-07 | 0.756068057 | 1.61111E-09 | 0.10637429 | 3.90003E-06 | |
| rc_AA412443_at | 287 | AA412443 | | 0.364026646 | 0.005904843 | 0.355261504 | 0.000673161 | 0.987349969 | 0.000639721 | |
| rc_AA417011_at | 292 | AA417011 | | 0.97881335 | 0.000103601 | 0.347607058 | 0.000209225 | 0.359543109 | 6.44615E-06 | |
| rc_AA417348_at | 293 | AA417348 | | 0.011726682 | 0.000513628 | 0.000733098 | 0.214868351 | 0.416407972 | 0.597824364 | |
| rc_AA417915_at | 294 | AA417915 | | 0.00031475 | 0.724609869 | 0.33434685 | 0.000849216 | 0.012345648 | 0.253561808 | |
| rc_AA418557_at | 295 | AA418557 | | 0.228039568 | 0.580130356 | 0.000535144 | 0.124915173 | 0.032252409 | 0.000643742 | |
| rc_AA421131_at | 298 | AA421131 | | 0.000944552 | 0.385647564 | 0.015545606 | 0.00033745 | 0.400009139 | 0.00441922 | |
| rc_AA421133_at | 299 | AA421133 | erythrocyte transmembrane protein | 0.048370115 | 0.776945443 | 3.5594E-06 | 0.170573072 | 0.011573179 | 0.000337276 | |
| rc_AA424037_s_ | 301 | AA424037 | | | 0.004243716 | 0.739593135 | 2.30322E-05 | 0.006963992 | 0.192467998 | 0.000122214 |
| rc_AA424245_at | 302 | AA424245 | | | 0.000912649 | 0.241386195 | 0.000606875 | 0.10233451 | 0.915105608 | 0.08414343 |
| rc_AA424515_at | 303 | AA424515 | | | 0.001461647 | 0.327161944 | 0.557700471 | 0.000331758 | 0.000350136 | 0.650111174 |
| rc_AA425325_at | 305 | AA425325 | | | 0.000137613 | 0.761000474 | 0.006888125 | 0.000531496 | 0.292230161 | 0.011066086 |
| rc_AA425354_at | 306 | AA425354 | | | 1.135E-05 | 0.848812392 | 4.31696E-05 | 0.000125249 | 0.776028887 | 0.000335665 |
| rc_AA426438_at | 309 | AA426438 | tissue factor pathway inhibitor (lipoprotein- associated coagulation inhibitor) | | 0.086215951 | 0.051460629 | 0.077775438 | 0.000971113 | 0.963651921 | 0.000841613 |
| rc_AA426454_s_ | 310 | AA426454 | imidazoline receptor candidate | | 4.93792E-06 | 0.168883843 | 0.000430545 | 0.013194044 | 0.320673843 | 0.1079437 |
| rc_AA427944_at | 313 | AA427944 | | | 0.016580683 | 2.63482E-05 | 0.961128446 | 0.040898728 | 0.020386125 | 4.53083E-05 |
| rc_AA428243_at | 314 | AA428243 | integrin beta 4 binding protein | | 0.000258966 | 0.030169371 | 0.000115376 | 0.338639919 | 0.847641147 | 0.260434676 |
| rc_AA428460_at | 316 | AA428460 | | | 0.369406205 | 2.86818E-05 | 0.170103625 | 1.87552E-06 | 0.031318989 | 0.00400089 |
| rc_AA429398_s_ | 317 | AA429398 | | | 0.042509423 | 0.318204908 | 0.000808205 | 0.00812556 | 0.209966492 | 0.000179435 |
| rc_AA430738_at | 322 | AA430738 | hypothetical protein FLJ22693 | | 2.4223E-05 | 0.512347676 | 0.057495876 | 3.43792E-05 | 0.027579258 | 0.027106503 |
| rc_AA433922_at | 326 | AA433922 | NRAS-related gene | | 0.000129534 | 0.750927276 | 0.024589837 | 0.000483913 | 0.13400345 | 0.029612486 |
| rc_AA435753_at | 329 | AA435753 | | | 0.167368191 | 0.01678153 | 0.00563702 | 0.000567982 | 0.188083313 | 4.20658E-06 |
| rc_AA435852_at | 331 | AA435852 | hypothetical protein | | 0.000178813 | 0.813799408 | 0.130706548 | 0.000825341 | 0.033909282 | 0.137866512 |
| rc_AA436244_at | 332 | AA436244 | | | 0.000347902 | 0.773066458 | 0.838936155 | 0.006955308 | 0.000335763 | 0.655473596 |
| rc_AA436489_at | 333 | AA436489 | dual specificity phosphatase 10 | | 0.089585972 | 0.000336423 | 0.53802583 | 0.042116461 | 0.028187175 | 7.58265E-05 |
| rc_AA436548_at | 334 | AA436548 | | | 4.79946E-05 | 0.79712195 | 0.073989554 | 0.000284052 | 0.03065051 | 0.082990101 |
| rc_AA436823_at | 338 | AA436823 | | | 3.43729E-06 | 0.007238466 | 0.000134014 | 0.199586541 | 0.434475995 | 0.550333062 |
| rc_AA436841_at | 339 | AA436841 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta | | 0.000757034 | 0.109130693 | 3.14861E-05 | 0.206545207 | 0.451070087 | 0.054341855 |
| rc_AA437226_s_ | 341 | AA437226 | interleukin 10 receptor, alpha | | 0.030634205 | 0.394007384 | 3.12463E-06 | 0.008853685 | 0.017676075 | 2.623E-06 |
| rc_AA442830_at | 342 | AA442830 | | | 0.277387057 | 0.000957882 | 0.739163222 | 4.56542E-05 | 0.474861158 | 0.000560401 |
| rc_AA446899_at | 348 | AA446899 | mannosidase, alpha, class 1B, member 1 | | 4.08376E-08 | 0.474845978 | 8.66417E-09 | 0.000104871 | 0.799444331 | 4.09828E-05 |
| rc_AA448228_at | 353 | AA448228 | HSPC142 protein | | 0.489815716 | 0.427628808 | 0.00011718 | 0.181303904 | 1.63664E-05 | 0.014570459 |
| rc_AA450073_s_ | 357 | AA450073 | paired mesoderm homeo box 1 | | 0.070060208 | 0.424331633 | 0.00057893 | 0.02291416 | 0.12207024 | 0.000282414 |
| rc_AA450373_at | 361 | AA450373 | | | 0.19184076 | 0.000421707 | 3.75092E-05 | 0.021344923 | 0.007526828 | 0.966348045 |
| rc_AA454016_at | 365 | AA454016 | | | 0.74223808 | 0.000765848 | 0.794392558 | 0.003084476 | 0.575990681 | 0.000561238 |
| rc_AA454928_at | 367 | AA454928 | phosphorylase kinase, beta | | 0.042150436 | 0.023733581 | 0.157838834 | 0.000111797 | 0.556629171 | 0.000814363 |
| rc_AA457148_at | 372 | AA457148 | | | 0.770822781 | 0.643699605 | 7.37551E-05 | 0.492232725 | 0.000493842 | 0.000182201 |
| rc_AA457407_at | 374 | AA457407 | transmembrane protease, serine 2 | | 0.322389783 | 0.009487182 | 0.088848624 | 0.000914536 | 0.499415786 | 9.30818E-05 |
| rc_AA457675_at | 376 | AA457675 | | | 0.000470812 | 0.007879992 | 0.000974653 | 0.721378015 | 0.850190113 | 0.848554875 |
| rc_AA459272_at | 377 | AA459272 | | | 8.59013E-05 | 0.738589634 | 0.711426345 | 0.003207799 | 0.00073865 | 0.989771621 |
| rc_AA460377_at | 378 | AA460377 | beta-catenin-interacting protein ICAT | | 0.015059101 | 0.036482503 | 0.009644184 | 5.52729E-05 | 0.881315511 | 3.13984E-05 |
| rc_AA464598_at | 387 | AA464598 | KIAA1389 protein | | 0.000373603 | 0.650628457 | 0.000200085 | 0.000684765 | 0.878718031 | 0.000416438 |
| rc_AA469954_at | 392 | AA469954 | | | 0.239197445 | 0.004848961 | 0.288136551 | 0.000228067 | 0.913292289 | 0.000330413 |
| rc_AA476594_i_ | 393 | AA476594 | Arg/Abl-interacting protein ArgBP2 | | 0.358342961 | 0.881892103 | 0.000846963 | 0.534258655 | 5.41111E-05 | 0.003508506 |
| rc_AA477119_at | 395 | AA477119 | | | 0.155425839 | 0.46185093 | 0.00021398 | 0.058896186 | 0.030447512 | 0.000152407 |
| rc_AA477833_at | 397 | AA477833 | translocase of inner mitochondrial membrane 44 (yeast) homolog | | 0.019542745 | 0.5471713 | 3.40147E-05 | 0.011694366 | 0.085999006 | 5.64814E-05 |
| rc_AA478615_s_ | 398 | AA478615 | H1 histone family, member X | | 0.640957846 | 0.0022057 | 0.208838599 | 0.000871626 | 0.453348417 | 6.70146E-05 |
| rc_AA478996_at | 401 | AA478996 | | | 0.680984202 | 0.000380025 | 0.977809564 | 0.000172484 | 0.677109345 | 0.000696316 |
| rc_AA481057_f_ | 404 | AA48105 | | | | | | | | |

TABLE 6 BPH vs. Normal and Cancer

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | |
|-----------------------------|---------------|------------|---|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| rc_aa482107_s_at | 406 | AA482107 | | 0.412141577 | 0.217724563 | 0.000197553 | 0.061952573 | 1.63874E-05 | 0.055779976 |
| rc_AA482559_at | 407 | AA482559 | RPA-binding trans-activator | 0.010341566 | 0.960678267 | 3.22844E-05 | 0.02919031 | 0.130837801 | 0.000454944 |
| rc_AA485243_at | 408 | AA485243 | leptin receptor | 3.17405E-05 | 0.744743793 | 0.400224468 | 0.00016024 | 0.001638049 | 0.311183055 |
| rc_AA488658_at | 413 | AA488658 | hypothetical protein | 0.000418682 | 0.365249562 | 0.186392502 | 0.000141589 | 0.036308821 | 0.048918937 |
| rc_AA488849_at | 414 | AA488849 | nucleotide binding protein 2 (E.coli MinD like) | 0.17603882 | 0.323192094 | 0.000687853 | 0.037989302 | 0.052798072 | 0.000161003 |
| rc_AA489637_at | 415 | AA489637 | | 0.003960452 | 0.871859148 | 0.000107388 | 0.010699848 | 0.346672042 | 0.000730896 |
| rc_AA490120_at | 416 | AA490120 | | 0.082001486 | 0.454413511 | 0.000859271 | 0.030324764 | 0.130537834 | 0.000479561 |
| rc_AA490520_at | 418 | AA490520 | | 0.00063489 | 0.471991068 | 0.445872157 | 0.000410063 | 0.011810787 | 0.185068096 |
| rc_AA490999_at | 420 | AA490999 | | 0.001846648 | 0.670951196 | 0.000150658 | 0.002708195 | 0.521238606 | 0.000368557 |
| rc_AA504255_at | 423 | AA504255 | ataxia telangiectasia and Rad3 related | 0.007747725 | 1.58087E-05 | 0.446946913 | 0.053347131 | 0.001163384 | 1.74835E-06 |
| rc_AA505022_at | 425 | AA505022 | | 0.250524892 | 0.000259519 | 0.084574205 | 7.98938E-06 | 0.584980634 | 7.63588E-07 |
| rc_AA599376_at | 435 | AA599376 | | 0.015748126 | 0.140670046 | 0.009272938 | 0.000615583 | 0.859099543 | 0.000343134 |
| rc_AA599443_f_at | 436 | AA599443 | hypothetical protein FLJ10595 | 0.379179145 | 0.00382066 | 0.40828628 | 0.000446702 | 0.960279666 | 0.000525999 |
| rc_AA609657_at | 446 | AA609657 | | 7.04465E-05 | 0.091053447 | 0.00093271 | 0.092251403 | 0.5283101 | 0.25823308 |
| rc_AA609848_at | 447 | AA609848 | | 0.042723584 | 0.092999102 | 0.036171711 | 0.000967007 | 0.948118344 | 0.000787862 |
| rc_AA609869_at | 448 | AA609869 | hypothetical protein FLJ13222 | 4.47677E-05 | 0.00053907 | 2.12675E-07 | 0.943295205 | 0.293840522 | 0.321292026 |
| rc_AA610070_at | 450 | AA610070 | calcium/calmodulin-dependent serine protein kinase (MAGUK family) | 0.000126016 | 0.058243496 | 0.558814317 | 0.170494931 | 2.76548E-05 | 0.021111632 |
| rc_AA620806_at | 453 | AA620806 | ASB-3 protein | 4.7861E-06 | 0.710135071 | 0.298838834 | 0.000563366 | 0.000797621 | 0.611912234 |
| rc_AA621325_at | 455 | AA621325 | HNK-1 sulfotransferase | 0.000848661 | 0.346193012 | 0.004864951 | 0.000232221 | 0.621405553 | 0.001162331 |
| rc_C14898_at | 467 | C14898 | | 0.000226586 | 0.885711705 | 6.82551E-05 | 0.003389818 | 0.77964221 | 0.001496457 |
| rc_C20547_at | 469 | C20547 | | 0.068260402 | 0.000952953 | 0.812550962 | 2.71206E-06 | 0.132387942 | 0.000746928 |
| rc_C20658_at | 470 | C20658 | cisplatin resistance-associated overexpressed protein | 0.000322792 | 0.311886375 | 0.000285103 | 7.37384E-05 | 0.975640568 | 6.58868E-05 |
| rc_D11789_f_at | 473 | D11789 | | 0.21798848 | 0.000243771 | 0.79113972 | 0.012426673 | 0.155631425 | 0.000180292 |
| rc_D11961_at | 475 | D11961 | hypothetical protein FLJ21343 | 0.066999427 | 0.031322113 | 0.050959636 | 0.000327468 | 0.909256528 | 0.000222056 |
| rc_D20085_at | 479 | D20085 | | 0.533566658 | 0.000441315 | 0.321182892 | 0.004260671 | 0.125585439 | 2.65015E-05 |
| rc_D52692_s_at | 497 | D52692 | Ca2+-dependent activator protein for secretion | 1.02115E-06 | 0.807110908 | 1.27404E-05 | 0.000127062 | 0.619779281 | 0.000681487 |
| rc_D60272_i_at | 499 | D60272 | | 0.000665091 | 0.000166097 | 0.000151004 | 0.431868883 | 0.714339713 | 0.641956827 |
| rc_D80298_f_at | 507 | D80298 | | 0.045427886 | 0.000323207 | 0.958861584 | 0.073418502 | 0.064448036 | 0.000644976 |
| rc_D80738_f_at | 509 | D80738 | | 0.190797369 | 0.00173762 | 0.245104642 | 4.17807E-05 | 0.889912758 | 7.00818E-05 |
| rc_F01684_at | 519 | F01684 | | 0.420181016 | 0.000494834 | 0.488322276 | 5.87948E-05 | 0.914533384 | 8.72831E-05 |
| rc_F02739_at | 525 | F02739 | | 5.54856E-05 | 0.053527575 | 0.000291424 | 0.133799091 | 0.698411971 | 0.246269511 |
| rc_F04019_at | 529 | F04019 | | 0.000166861 | 0.000950517 | 0.555841593 | 0.965823573 | 0.00259065 | 0.007252422 |
| rc_F10193_at | 539 | F10193 | chromosome 21 open reading frame 39 | 1.30777E-05 | 0.948962688 | 0.020624022 | 0.000363518 | 0.05248761 | 0.062247376 |
| rc_F10323_f_at | 540 | F10323 | retinoblastoma-like 2 (p130) | 0.000650946 | 0.502771636 | 0.015425251 | 0.000500148 | 0.348990394 | 0.007831047 |
| rc_F10980_at | 541 | F10980 | | 8.9375E-05 | 0.653407439 | 0.012465868 | 0.000223205 | 0.178217348 | 0.012058063 |
| rc_H01068_at | 543 | H01068 | | 0.86517363 | 0.000569676 | 0.466764828 | 0.001528575 | 0.394499429 | 9.00281E-05 |
| rc_H09077_at | 551 | H09077 | | 3.06359E-05 | 1.2292E-05 | 0.021919052 | 0.46401342 | 0.07497746 | 0.021793621 |
| rc_H11463_at | 552 | H11463 | inhibitor of growth family, member 3 | 0.00061851 | 0.000440258 | 0.000113152 | 0.597222623 | 0.678354487 | 0.869200328 |
| rc_H14810_s_at | 553 | H14810 | popeye protein 3 | 1.36532E-05 | 0.832182578 | 0.004057496 | 0.000637115 | 0.161519166 | 0.028710637 |
| rc_H18099_at | 560 | H18099 | | 0.247088588 | 0.003400663 | 0.301565366 | 0.000158641 | 0.90607919 | 0.000239103 |
| rc_H23407_s_at | 565 | H23407 | MAD1 (mitotic arrest deficient, yeast, homolog)-like 1 | 0.000753122 | 0.112093793 | 2.71462E-05 | 0.201584279 | 0.432877141 | 0.049424886 |
| rc_H23520_at | 566 | H23520 | | 0.611355729 | 0.000871266 | 0.849483973 | 0.000293132 | 0.507906287 | 0.002361124 |
| rc_H38418_at | 570 | H38418 | | 0.185134143 | 0.065592241 | 0.008782561 | 0.50515013 | 0.000181804 | 7.8388E-05 |
| rc_H38995_f_at | 571 | H38995 | KIAA0471 gene product | 0.009631356 | 0.97045862 | 5.86902E-05 | 0.028554385 | 0.175136692 | 0.000728104 |
| rc_H45265_at | 574 | H45265 | ATP-binding cassette, sub-family A (ABC1), member 7 | 0.000152193 | 4.19671E-07 | 0.003258301 | 0.08727525 | 0.422648726 | 0.015812939 |
| rc_H48263_at | 575 | H48263 | | 0.185258234 | 0.007096561 | 0.191295818 | 0.00022522 | 0.986389253 | 0.000238835 |
| rc_H48475_at | 576 | H48475 | ribosomal protein L37a | 0.227463546 | 0.00062116 | 0.579381783 | 1.76941E-05 | 0.535824365 | 0.000177441 |
| rc_H58781_at | 582 | H58781 | | 0.042650671 | 0.000369904 | 0.497627082 | 0.082860732 | 0.010272658 | 6.73936E-05 |
| rc_H59141_at | 584 | H59141 | hypothetical protein | 0.001248184 | 4.64747E-07 | 0.066732688 | 0.031003204 | 0.185981631 | 0.000909745 |
| rc_H63994_at | 588 | H63994 | | 0.042052556 | 0.003078049 | 0.051932289 | 5.75286E-06 | 0.93248223 | 8.15902E-06 |
| rc_H64411_at | 589 | H64411 | KIAA0618 gene product | 0.01802462 | 0.0 | | | | |

TABLE 6 BPH vs. Normal and Cancer

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | |
|-----------------------------|---------------|------------|---|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| rc_H77531_s_at | 593 | H77531 | HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A | 0.000791123 | 0.49434307 | 0.184056577 | 0.00056294 | 0.054421223 | 0.078090378 |
| rc_H97868_at | 608 | H97868 | | 0.322057918 | 0.489184724 | 0.000285548 | 0.136645099 | 0.012333089 | 0.000230315 |
| rc_H97889_at | 609 | H97889 | | 0.158642014 | 0.00916284 | 0.299358664 | 0.000236375 | 0.724266848 | 0.00075937 |
| rc_H98676_at | 610 | H98676 | | 0.127756769 | 0.002896791 | 0.262913685 | 3.64577E-05 | 0.701889069 | 0.000148754 |
| rc_N20967_at | 717 | N20967 | | 9.92879E-05 | 0.817666422 | 3.00688E-05 | 0.000539948 | 0.790070901 | 0.000221099 |
| rc_N22115_s_at | 720 | N22115 | KIAA0447 gene product | 5.18274E-07 | 0.014513808 | 3.98659E-05 | 0.067547386 | 0.387363889 | 0.284673955 |
| rc_N22297_f_at | 721 | N22297 | | 0.054494667 | 0.052949003 | 0.08027668 | 0.000541487 | 0.869037035 | 0.000917296 |
| rc_N32521_at | 735 | N32521 | hypothetical protein FLJ11085 | 0.547891484 | 0.041933612 | 0.000238523 | 0.014113039 | 0.003549591 | 5.39907E-07 |
| rc_N34517_s_at | 738 | N34517 | integrin, alpha 7 | 0.005879801 | 0.196182153 | 0.004385481 | 0.00040993 | 0.928485921 | 0.000303466 |
| rc_N38882_at | 741 | N38882 | | 0.014629787 | 0.005666897 | 0.251351421 | 0.530957263 | 0.000663242 | 0.000303436 |
| rc_N51579_at | 748 | N51579 | transporter-like protein | 0.44766874 | 6.17952E-05 | 0.962144968 | 0.001295779 | 0.499475206 | 0.900139415 |
| rc_N54053_at | 752 | N54053 | secreted phosphoprotein 2, 24kD | 0.116492665 | 0.015273471 | 0.039361645 | 0.00027615 | 0.641546757 | 5.23218E-05 |
| rc_N54845_at | 753 | N54845 | | 0.000443555 | 0.073889565 | 0.000793416 | 0.227981278 | 0.881125278 | 0.282635582 |
| rc_N55085_at | 754 | N55085 | | 0.220208071 | 0.876075911 | 0.000843717 | 0.384166413 | 1.49242E-05 | 0.003419797 |
| rc_N59862_at | 760 | N59862 | | 0.462122243 | 0.001300248 | 0.278791676 | 0.000214232 | 0.741521525 | 6.58223E-05 |
| rc_N66001_at | 765 | N66001 | mouse double minute 4, human homolog of; p53-binding protein | 0.269409972 | 0.001627722 | 0.449591713 | 7.93964E-05 | 0.741058833 | 0.000255792 |
| rc_N66053_f_at | 766 | N66053 | butyrophilin, subfamily 3, member A1 | 0.000767668 | 0.638609685 | 0.000120387 | 0.018876455 | 0.648066184 | 0.005990603 |
| rc_N67108_at | 769 | N67108 | | 2.22447E-05 | 0.94547199 | 0.335823565 | 0.000534028 | 0.00186846 | 0.462281008 |
| rc_N67324_at | 770 | N67324 | | 0.061297249 | 0.015332682 | 0.029486337 | 0.000101757 | 0.771895611 | 3.46367E-05 |
| rc_N67899_at | 774 | N67899 | | 8.19817E-05 | 0.845939057 | 0.027139019 | 0.000532728 | 0.100944503 | 0.04285656 |
| rc_N80693_at | 787 | N80693 | | 0.798568519 | 0.000819546 | 0.654401168 | 0.002677747 | 0.504907369 | 0.000334108 |
| rc_N89827_at | 788 | N89827 | RALBP1 associated Eps domain containing 2 | 0.129696038 | 0.000403735 | 8.58239E-05 | 0.032513633 | 0.022112053 | 0.895818166 |
| rc_N93495_at | 795 | N93495 | uncharacterized hematopoietic stem/progenitor cells protein MDS033 | 0.082365924 | 0.047090947 | 0.00063645 | 0.000799522 | 0.111310122 | 2.03892E-06 |
| rc_R00440_at | 802 | R00440 | ancient conserved domain protein 4 | 0.538637852 | 6.90248E-05 | 0.927092838 | 0.000926675 | 0.619532275 | 0.000178704 |
| rc_R17000_s_at | 812 | R17000 | NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase) | 0.000151792 | 0.075089669 | 0.000101925 | 0.149353698 | 0.926045731 | 0.12770179 |
| rc_R25116_at | 813 | R25116 | | 0.0420832 | 0.03125809 | 0.026701279 | 0.000169518 | 0.862052816 | 9.11635E-05 |
| rc_R40030_at | 827 | R40030 | hypothetical protein FLJ20047 | 0.567472456 | 0.000280009 | 0.804462147 | 0.002571098 | 0.436977215 | 0.000218515 |
| rc_R41798_s_at | 829 | R41798 | KIAA1374 protein | 0.000373432 | 0.706910506 | 0.012448736 | 0.000894251 | 0.315054178 | 0.014659398 |
| rc_R42336_s_at | 831 | R42336 | | 0.70873782 | 2.16988E-05 | 0.77916386 | 0.000163747 | 0.929588049 | 0.000119701 |
| rc_R42525_at | 833 | R42525 | | 0.050001405 | 0.071849508 | 0.013930003 | 0.000778775 | 0.635857474 | 0.000159677 |
| rc_R56216_at | 845 | R56216 | | 0.000821825 | 0.352494161 | 0.151440792 | 0.0002362 | 0.069860079 | 0.036903476 |
| rc_R66690_at | 851 | R66690 | | 0.548034357 | 0.001498849 | 0.392082801 | 0.000384981 | 0.808745096 | 0.000168251 |
| rc_R70212_s_at | 853 | R70212 | CD79A antigen (immunoglobulin-associated alpha) | 0.001627385 | 0.92358255 | 1.96242E-05 | 0.011419498 | 0.28878538 | 0.000540241 |
| rc_R82942_s_at | 856 | R82942 | | 4.27278E-06 | 0.038346252 | 9.40527E-05 | 0.06641734 | 0.511382181 | 0.207797821 |
| rc_R84968_at | 858 | R84968 | | 0.029165843 | 9.17654E-05 | 0.74623486 | 0.052010697 | 0.078018241 | 0.0004854 |
| rc_R89291_at | 861 | R89291 | | 0.000287625 | 0.129809655 | 0.120359785 | 7.72734E-06 | 0.049234398 | 0.005999323 |
| rc_R92737_at | 864 | R92737 | aquaporin 3 | 0.045317535 | 0.54600908 | 0.000762777 | 0.024731156 | 0.195577177 | 0.000722979 |
| rc_T15530_at | 879 | T15530 | | 0.039751248 | 0.193908111 | 0.000219396 | 0.003085344 | 0.119916961 | 1.53896E-05 |
| rc_T16556_at | 882 | T16556 | | 0.547027876 | 0.000735355 | 0.131501406 | 0.006096912 | 0.045271057 | 6.8433E-06 |
| rc_T49291_s_at | 895 | T49291 | lymphocyte-specific protein 1 | 0.023580272 | 0.159004442 | 0.000765019 | 0.00120856 | 0.296144015 | 3.27932E-05 |
| rc_T50387_at | 897 | T50387 | | 0.685476265 | 0.000770227 | 0.324729565 | 0.003799426 | 0.187347142 | 5.10594E-05 |
| rc_T53404_at | 898 | T53404 | hypothetical protein from clone 643 | 0.47780256 | 0.003673041 | 0.259379562 | 0.000720609 | 0.69168737 | 0.000191916 |
| rc_T54613_at | 900 | T54613 | | 5.52684E-05 | 0.022747185 | 0.000284729 | 0.24335011 | 0.701984774 | 0.40594297 |
| rc_T54617_at | 901 | T54617 | | 0.857947447 | 4.07249E-05 | 0.397904433 | 0.000148584 | 0.527265593 | 0.001199664 |
| rc_T65802_at | 908 | T65802 | | 0.012663512 | 0.532196596 | 0.000313482 | 0.007483397 | 0.291974796 | 0.000319721 |
| rc_T79868_f_at | 915 | T79868 | hypothetical protein 384D8_6 | 0.071499128 | 0.033264086 | 0.074047238 | 0.000392669 | 0.987909984 | 0.000412941 |
| rc_T82292_s_at | 916 | T82292 | protease, serine, 11 (IGF binding) | 0.000399556 | 0.678142361 | 0.051597503 | 0.000824339 | 0.130506724 | 0.043561586 |
| rc_T86121_at | 918 | T86121 | | 0.013631945 | 0.898945913 | 2.7658E-06 | 0.029665506 | 0.035142628 | 5.76483E-05 |
| rc_T87533_at | 920 | T87533 | | 0.989160192 | 0.000472522 | 0.640089183 | 0.000751611 | 0.648053004 | 0.002981136 |

TABLE 6 BPH vs. Normal and Cancer
1669495.1

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | |
|-----------------------------|---------------|------------|--|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| rc_T90038_f_at | 924 | T90038 | butyrophilin, subfamily 3, member A2;butyrophilin, subfamily 3, member A3 | 4.93914E-06 | 0.243601757 | 8.38948E-05 | 0.007362582 | 0.547300658 | 0.031384668 |
| rc_T99373_at | 934 | T99373 | | 0.026021837 | 3.07604E-06 | 0.711043501 | 0.008523742 | 0.078371167 | 2.98773E-05 |
| rc_W37384_i_at | 1001 | W37384 | non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase) | 0.000625839 | 0.217732697 | 0.000147234 | 0.096608548 | 0.7216482 | 0.048383963 |
| rc_W42483_at | 1003 | W42483 | hypothetical protein similar to mouse Dnajl1 | 2.97466E-05 | 0.676684762 | 0.031770051 | 0.000106724 | 0.05435082 | 0.028721568 |
| rc_W44558_s_at | 1005 | W44558 | adaptor-related protein complex 1, sigma 1 subunit | 0.079864992 | 0.042988764 | 0.034848175 | 0.000669599 | 0.73367308 | 0.000215475 |
| rc_W60649_at | 1019 | W60649 | | 0.023339325 | 0.129224665 | 0.006757142 | 0.000824018 | 0.675851904 | 0.000206179 |
| rc_W80509_s_at | 1032 | W80509 | death associated transcription factor 1 | 0.000271744 | 0.148881601 | 0.000426903 | 0.10048575 | 0.910884693 | 0.122505852 |
| rc_W86660_at | 1034 | W86660 | | 0.150249394 | 6.18841E-06 | 0.557722374 | 0.001658036 | 0.418699422 | 0.000115844 |
| rc_W93396_at | 1038 | W93396 | | 0.000180228 | 0.540603359 | 0.319667744 | 0.00021213 | 0.009081674 | 0.156804025 |
| rc_Z38551_s_at | 1107 | Z38551 | hypothetical protein FLJ10210 | 0.007617909 | 0.125060522 | 0.00394587 | 0.000220695 | 0.839190935 | 0.000107925 |
| rc_Z39874_at | 1110 | Z39874 | | 0.018342738 | 0.000251552 | 0.969844211 | 0.120049181 | 0.022998914 | 0.000387407 |
| rc_Z40012_f_at | 1113 | Z40012 | NCK-associated protein 1 | 0.038639336 | 0.043854062 | 0.05138364 | 0.000255085 | 0.909554475 | 0.000374451 |
| rc_Z40332_at | 1115 | Z40332 | vesicle docking protein p115 | 0.028012659 | 0.10943539 | 0.012529791 | 0.000762549 | 0.7761268 | 0.000299824 |
| rc_Z41763_at | 1120 | Z41763 | | 6.03127E-05 | 0.82776366 | 0.002670862 | 0.00038983 | 0.338788944 | 0.006770727 |
| S75463_at | 871 | S75463 | Tu translation elongation factor, mitochondrial | 0.000271911 | 0.000533911 | 0.00172916 | 0.765671272 | 0.63019533 | 0.471338415 |
| S77154_s_at | 872 | S77154 | nuclear receptor subfamily 4, group A, member 2 | 0.720602576 | 0.932154297 | 5.84424E-05 | 0.829150677 | 0.000513773 | 0.001105408 |
| T40327_s_at | 891 | T40327 | electron-transferring-flavoprotein dehydrogenase | 7.27596E-06 | 0.215221988 | 0.819260055 | 0.011040692 | 7.74754E-06 | 0.167330005 |
| T89243_s_at | 922 | T89243 | KIAA1243 protein | 0.00081408 | 0.517949226 | 0.114764867 | 0.000657245 | 0.092965856 | 0.053186849 |
| U00672_at | 935 | U00672 | interleukin 10 receptor, alpha | 0.000287943 | 0.609290849 | 1.66617E-06 | 0.011540026 | 0.269359727 | 0.000474683 |
| U03272_at | 937 | U03272 | fibrillin 2 (congenital contractual arachnodactyly) | 0.000310928 | 0.332521737 | 0.209649826 | 8.44451E-05 | 0.025692948 | 0.04828388 |
| U04811_at | 939 | U04811 | trophinin | 1.5625E-05 | 0.755433375 | 0.054905474 | 0.000984445 | 0.022792101 | 0.194301082 |
| U04811_at | 939 | U04811 | trophinin | 2.20509E-06 | 0.327834193 | 0.000136465 | 0.002712738 | 0.383208442 | 0.025499623 |
| U09366_at | 943 | U09366 | zinc finger protein 133 (clone pHZ-13) | 0.000213171 | 0.5068558 | 0.610825511 | 0.000200267 | 0.002444941 | 0.288631384 |
| U11861_at | 945 | U11861 | maternal G10 transcript | 0.000482828 | 0.00167301 | 9.90184E-05 | 0.90794872 | 0.702310162 | 0.826191525 |
| U12775_at | 946 | U12775 | agouti (mouse)-signaling protein | 0.000271316 | 0.000844452 | 0.000473875 | 0.859392382 | 0.889729458 | 0.765131751 |
| U13220_at | 947 | U13220 | forkhead box F2 | 0.000592743 | 0.851887641 | 3.88357E-05 | 0.007392289 | 0.519237 | 0.001178975 |
| U13991_at | 948 | U13991 | TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD | 1.45014E-06 | 0.006140037 | 1.01255E-06 | 0.168790439 | 0.946149483 | 0.151190281 |
| U15932_at | 949 | U15932 | dual specificity phosphatase 5 | 0.877505283 | 0.806495835 | 1.85723E-05 | 0.914714787 | 2.57739E-05 | 0.000146058 |
| U23852_s_at | 954 | U23852 | lymphocyte-specific protein tyrosine kinase | 0.015926444 | 0.891018698 | 9.08522E-05 | 0.032567274 | 0.153847965 | 0.000703723 |
| U25265_at | 957 | U25265 | mitogen-activated protein kinase kinase 5 | 8.86395E-06 | 0.005417963 | 5.93432E-05 | 0.305372601 | 0.684875389 | 0.503461673 |
| U26174_at | 959 | U26174 | granzyme K (serine protease, granzyme 3; tryptase II) | 3.92686E-05 | 0.206902143 | 0.000598254 | 0.027205202 | 0.519267093 | 0.10031708 |
| U32674_s_at | 962 | U32674 | G protein-coupled receptor 9 | 0.003147245 | 0.1818672 | 0.076391484 | 0.000184255 | 7.37649E-06 | 0.847933992 |
| U40372_at | 963 | U40372 | phosphodiesterase 1C, calmodulin-dependent (70kD) | 0.284766484 | 1.17113E-05 | 0.46702597 | 0.000897191 | 0.745348724 | 0.000311221 |
| U43527_at | 966 | U43527 | KiSS-1 metastasis-suppressor | 0.068750933 | 0.878566298 | 0.000141006 | 0.096679594 | 0.059509384 | 0.000920023 |
| U46006_s_at | 968 | U46006 | cysteine and glycine-rich protein 2 | 0.000581958 | 0.677096089 | 0.000421368 | 0.013813896 | 0.93464395 | 0.011277242 |

TABLE 6 BPH vs. Normal and Cancer

| Affymetrix Fragment Name | SEQ ID NO: | GenBank ID | GenBank Name | P- Values | | | | | |
|-----------------------------|---------------|------------|--|---------------------|----------------------|----------------------|---------------------|---------------------|----------------------|
| | | | | Normal vs. BPHWS | Normal vs. BPHNoS | Normal vs. Cancer | BPHWS vs. BPHNoS | BPHWS vs. Cancer | BPHNoS vs. Cancer |
| U52112_ma1_at | 969 | U52112 | L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraparesis 1) | 0.012256648 | 0.603209864 | 0.000361314 | 0.009782964 | 0.313616052 | 0.000525936 |
| U55209_at | 973 | U55209 | myosin VIIA (Usher syndrome 1B (autosomal recessive, severe)) | 0.026307797 | 0.000534284 | 5.50778E-05 | 0.139252083 | 0.085728294 | 0.977237559 |
| U57623_s_at | 975 | U57623 | fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) | 0.000249597 | 0.006076702 | 2.31411E-07 | 0.680669423 | 0.152138423 | 0.095412354 |
| U58522_at | 976 | U58522 | huntingtin interacting protein 2 | 0.950874668 | 0.000404266 | 0.026015373 | 0.000816174 | 0.04004298 | 0.12201215 |
| U66075_at | 980 | U66075 | GATA-binding protein 6 | 0.000177786 | 0.094949773 | 5.41966E-05 | 0.129840147 | 0.784613111 | 0.079354568 |
| U66615_at | 981 | U66615 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 | 0.00427057 | 0.860602352 | 0.000125812 | 0.01088834 | 0.353965999 | 0.000781605 |
| U89922_s_at | 987 | U89922 | lymphotoxin beta (TNF superfamily, member 3) | 0.081431989 | 0.705262065 | 1.14225E-05 | 0.069803458 | 0.012069263 | 5.95219E-05 |
| W52493_at | 1013 | W52493 | protein kinase C, beta 1 | 4.17744E-05 | 0.407939223 | 0.47764998 | 2.61848E-05 | 0.001311163 | 0.165780725 |
| X06318_at | 1048 | X06318 | nuclear transport factor 2 (placental protein 15) | 4.53981E-05 | 0.309598889 | 0.000193355 | 0.01564851 | 0.739435449 | 0.033561473 |
| X07315_at | 1053 | X07315 | lysozyme (renal amyloidosis) | 0.00096734 | 0.024484461 | 0.000991289 | 0.558914618 | 0.994799819 | 0.56276584 |
| X14008_rna1_f_at | 1056 | X14008 | CD37 antigen | 0.047298803 | 0.921767172 | 1.2563E-05 | 0.081015792 | 0.023720356 | 0.000192698 |
| X14046_at | 1057 | X14046 | cholinergic receptor, nicotinic, beta polypeptide 1 (muscle) | 0.032116442 | 0.896768704 | 6.54708E-06 | 0.097237805 | 0.024859085 | 0.000287679 |
| X14830_at | 1058 | X14830 | vav 1 oncogene | 0.936178672 | 0.000286907 | 0.137976127 | 0.000630986 | 0.183095639 | 0.024428637 |
| X16316_at | 1059 | X16316 | DNA segment on chromosome 12 (unique) | 0.005646314 | 0.4794965 | 0.000157845 | 0.002861938 | 0.337620027 | 0.00013174 |
| X54870_at | 1065 | X54870 | 2489 expressed sequence | 0.000450913 | 0.241248516 | 0.00029577 | 0.07293822 | 0.916408 | 0.059393045 |
| X58529_at | 1070 | X58529 | immunoglobulin heavy constant mu | 0.026942297 | 0.975028968 | 5.32141E-08 | 0.070184957 | 0.002196974 | 6.90925E-06 |
| X60673_s_at | 1072 | X60673 | adenylate kinase 3 | 0.014055428 | 1.64563E-05 | 0.000854329 | 0.036097108 | 0.40449053 | 0.17235001 |
| X63741_s_at | 1074 | X63741 | early growth response 3 | 0.050166995 | 0.302932401 | 1.63652E-08 | 0.522269647 | 0.000467351 | 0.000208487 |
| X66358_at | 1079 | X66358 | cyclin-dependent kinase-like 1 (CDC2-related kinase) | 3.6744E-05 | 0.079324094 | 3.35901E-05 | 0.080441339 | 0.984409054 | 0.077518373 |
| X66839_at | 1080 | X66839 | carbonic anhydrase IX | 3.93574E-06 | 0.662915937 | 0.008885816 | 0.000624117 | 0.057988735 | 0.078713562 |
| X68277_at | 1082 | X68277 | dual specificity phosphatase 1 | 0.003463894 | 0.023542489 | 5.00933E-13 | 0.79747022 | 4.48312E-05 | 0.000125081 |
| X72882_at | 1084 | X72882 | hypothetical protein FLJ10747,tumor necrosis factor receptor | 0.000586574 | 1.73881E-05 | 0.061863645 | 0.20511364 | 0.136254698 | 0.010057929 |
| X75962_at | 1085 | X75962 | superfamily, member 4 | 1.07753E-05 | 0.259082214 | 0.000322398 | 2.07333E-06 | 0.445393473 | 4.56511E-05 |
| X83705_s_at | 1089 | X83705 | platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) | 0.000211219 | 0.000641028 | 0.003169595 | 0.843987656 | 0.474177301 | 0.409652768 |
| X96584_at | 1096 | X96584 | nephroblastoma overexpressed gene | 0.000449835 | 0.36091834 | 0.013539811 | 0.00014621 | 0.323949108 | 0.003364493 |
| X99142_at | 1097 | X99142 | keratin, hair, basic, 6 (monilethrix) | 0.104620098 | 0.022019682 | 0.075077447 | 0.00038452 | 0.881497721 | 0.000232112 |
| Y07595_at | 1099 | Y07595 | general transcription factor IIH, polypeptide 4 (52kD subunit) | 0.000268402 | 0.028695565 | 5.26844E-05 | 0.352269642 | 0.704788647 | 0.206775434 |
| Y09022_at | 1102 | Y09022 | Not56 (D. melanogaster)-like protein | 0.000142024 | 0.084289616 | 0.000108418 | 0.131801466 | 0.949831739 | 0.118236485 |
| Z35093_at | 1105 | Z35093 | surfeit 1 | 0.000740458 | 0.015177247 | 0.000173743 | 0.635076989 | 0.718277145 | 0.428942461 |

Table 7

| | Prostatic tissues | Cell Line | | | |
|----------------------|----------------------|-----------|---------|-------|-------|
| | | BRF-55T | PZ-HPV7 | BPH-1 | LNCaP |
| Up-regulated genes | 61 | 33 | 22 | 20 | 20 |
| Down-regulated genes | 43 | 31 | 28 | 30 | 33 |
| Total | 104 | 64 | 50 | 50 | 53 |